

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 04:17:29 ; Search time 3155.99 Seconds
(without alignments)
9405.294 Million cell updates/sec

Title: US-09-864-675-1
Perfect score: 994
Sequence: 1 atgaggcgcgacccggcccc.....caccttggaattgaattaaa 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match Length DB	ID		
	1	674	67.8	805	12	BI918620
	2	586	59.0	1047	12	BM914622
c	3	467.2	47.0	1041	12	BI412864
	4	467	47.0	524	13	BX281777
	5	404	40.6	549	9	AA706226
	6	395.6	39.8	412	9	AI041451
	7	381	38.3	488	13	BX529505
	8	363.8	36.6	427	10	BF108794
c	9	317.4	31.9	949	12	BI410828
	10	272.6	27.4	795	12	BI651936
	11	234.4	23.6	333	10	BE983573
	12	232.2	23.4	529	10	AW476657
	13	224	22.5	297	9	AA772412
c	14	180	18.1	362	13	BX089049
	15	171.8	17.3	256	10	AW762061
	16	154	15.5	657	13	BQ078813
	17	151.8	15.3	259	10	BE648780
	18	151.4	15.2	327	9	AA968077
c	19	145	14.6	539	9	AL918370
	20	109	11.0	458	9	AI152190
	21	105.2	10.6	750	28	BZ847665
	22	101	10.2	493	28	BH057870
c	23	100.4	10.1	481	28	AZ987593
c	24	97.4	9.8	180	29	CE103297
	25	90.2	9.1	243	10	BB570162
c	26	83.6	8.4	512	9	AI073386
	27	81.2	8.2	167	9	AI836531
	28	76.6	7.7	477	10	BE984041
	29	72.8	7.3	761	13	BX876483
	30	68.4	6.9	769	12	BI413085
	31	67.2	6.8	765	12	BI522417
	32	67.2	6.8	818	12	BI651928
	33	66	6.6	751	29	CNS04J6G
	34	64.8	6.5	321	10	BE983721
	35	64.4	6.5	538	9	AL925790
c	36	61	6.1	491	9	AL909688
	37	60.4	6.1	363	29	CE326275
	38	60.4	6.1	413	14	N62228
c	39	60.2	6.1	322	9	AL909689
	40	59	5.9	356	29	CG614660
	41	58.4	5.9	685	14	CA351220
	42	53	5.3	1630	11	AK051824
	43	51.6	5.2	925	29	CNS0091P
c	44	51.6	5.2	982	13	BX415111
	45	50.8	5.1	647	12	BI960178

ALIGNMENTS

RESULT 1
 BI918620
 LOCUS BI918620 805 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603176570F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240969 5',
 mRNA sequence.
 ACCESSION BI918620
 VERSION BI918620.1 GI:16182295
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 805)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11607 row: k column: 18
 High quality sequence start: 2
 High quality sequence stop: 778.
 FEATURES Location/Qualifiers
 source 1. .805
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5240969"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_121"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
 fetal brains, female age 20 weeks, female age 24 weeks,
 and male age 26 weeks. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 0.7-3.5 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 017. Note:
 this is a NIH_MGC Library."
 ORIGIN
 Query Match 67.8%; Score 674; DB 12; Length 805;
 Best Local Similarity 98.7%; Pred. No. 2.3e-130;
 Matches 732; Conservative 0; Mismatches 5; Indels 5; Gaps 5;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGC-TTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTG 59
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 Db 64 ATGAGGCGCGACCCGGCCCCCGCGTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTG 123
 Qy 60 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTTGGTGGTGGGA 119
 |||
 Db 124 CTACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTTGGTGGTGGGA 183
 Qy 120 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 179
 |||
 Db 184 GGGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCC 243
 Qy 180 GCCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 239
 |||
 Db 244 GCCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGG 303
 Qy 240 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 299
 |||
 Db 304 GGGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCA 363
 Qy 300 GCGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTG- 358
 |||
 Db 364 GCGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGT 423
 Qy 359 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 418
 |||
 Db 424 CCCCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTG 483
 Qy 419 ACTGCGCCACCCGGGCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGA 478
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 Db 484 ACTGCGCCACCCGGGCCAAGTTGAAGAAGATGACGAGCCAGACGGGACAGGTGGGTGAGA 543
 Qy 479 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCA 538
 |||
 Db 544 AGCAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCA 603
 Qy 539 AGGATGGCAAGGAGCTCAACCG-CAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 597
 |||
 Db 604 AGGATGGCAAGGAGCTCAACCGTCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGA 663
 Qy 598 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGA-GTATGTCTG 656
 |||
 Db 664 AAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGGTATGTCTG 723
 Qy 657 CGAGG-CCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCG 715
 |||
 Db 724 CGAGGCCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGTTTTACGTCAACAGGT 783
 Qy 716 TGAGCACCACCCTGTCATCCTG 737
 |||
 Db 784 TGAGCACCAACCTGTCATCCTG 805

RESULT 2

BM914622

LOCUS BM914622 1047 bp mRNA linear EST 12-MAR-2002

DEFINITION AGENCOURT_6615334 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480308

5', mRNA sequence.

ACCESSION BM914622

VERSION BM914622.1 GI:19365001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1047)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM2002 row: p column: 05
High quality sequence stop: 541.

FEATURES
source Location/Qualifiers
1. .1047
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5480308"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 59.0%; Score 586; DB 12; Length 1047;
Best Local Similarity 98.2%; Pred. No. 6.4e-112;
Matches 603; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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QY      272 GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTCCTGGAGCCCACGGAAC 331
          |||
Db       1 GCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTTCCTGGAGCCCACGGAAC 60

QY      332 AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCCTCGATACCAACGGCAAAAATCTCAAGA 391
          |||
Db       61 AGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCCTCGATACCAACGGCAAAAATCTCAAGA 120

QY      392 AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA 451
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Db      121 AAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCAAGTTGAAGAAGATGA 180

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Qy 452 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTA 511
 |||
 Db 181 AGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTA 240
 Qy 512 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 571
 |||
 Db 241 ATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACA 300
 Qy 572 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 631
 |||
 Db 301 TTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGG 360
 Qy 632 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 691
 |||
 Db 361 TGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCC 420
 Qy 692 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAGCCCC 751
 |||
 Db 421 GGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAGCCCC 480
 Qy 752 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCG 811
 |||
 Db 481 GGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGCTGCTACTACATCG 540
 Qy 812 AGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGTTT-G 870
 |||
 Db 541 AGGCCATCAATCAGCTTTCCTGCAAATGTCCCAATGGATTCTTCGGACCAACATGTTTGG 600
 Qy 871 GAGAAACTGCCTTT 884
 |||
 Db 601 GAGAAACTGCCCTT 614

RESULT 3

BI412864/c

LOCUS BI412864 1041 bp mRNA linear EST 14-AUG-2001

DEFINITION 602988202F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5144016 5', mRNA sequence.

ACCESSION BI412864

VERSION BI412864.1 GI:15173787

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1041)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

```

FEATURES             Location/Qualifiers
     source            1. .1041
                        /organism="Mus musculus"
                        /mol_type="mRNA"
                        /strain="Czech II"
                        /db_xref="taxon:10090"
                        /clone="IMAGE:5144016"
                        /tissue_type="pooled lung tumors"
                        /lab_host="DH10B (phage-resistant)"
                        /clone_lib="NCI_CGAP_Lu33"
                        /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCGCCTCTGTTTTTTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

Query Match 47.0%; Score 467.2; DB 12; Length 1041;
Best Local Similarity 86.6%; Pred. No. 4.4e-87;
Matches 563; Conservative 0; Mismatches 78; Indels 9; Gaps 4;

[illegible]

Db 296 AGCCCTCCTATCGCTGGTTCAAGGATGGCAAGGAAGTCAACCGGAGTCGTGATATTCGCA 237
 QY 578 TCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGG 637
 |||| ||||||| ||||||||||||||| ||||||||||||||| |||| |||||||
 Db 236 TCAAGTATGGCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAGTGAGGGTGGAGG 177
 QY 638 ACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGGCC 697
 | || ||||||| |||| ||||||||||||||| ||||||||||||||| |||||||
 Db 176 ATGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCGTGAGGGGCC 117
 QY 698 GGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGT 757
 | || | ||||||||||||||||||| ||||||||||||||| || |||||||||
 Db 116 GACTCCATGTCAACAGCGTGAGCACCCTCTGTCATCCTGGTCGGGACATGCCCGGAAGT 57
 QY 758 GCAACGAGACAGCCAAGTCCTA--TTGCGTCAATGGAGGCGTCTGCTACT 805
 |||| ||||| ||||||||||| || || ||||||||||| |||||||
 Db 56 GCAATGAGACCGCCAAGTCCTACCATGTGTGAATGGAGGCGTGTGCTACT 7

RESULT 4

BX281777

LOCUS BX281777 524 bp mRNA linear EST 04-MAR-2003

DEFINITION BX281777 NIH_MGC_121 Homo sapiens cDNA clone IMAGp998K1811607 ;
IMAGE:5240969, mRNA sequence.

ACCESSION BX281777

VERSION BX281777.1 GI:28612804

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 524)

AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.

TITLE Human UnigeneSet - RZPD3

JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998K1811607.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)

[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13u, Primer sequence: CGTTGTAAACGACGGCCAGT.

FEATURES

source

Location/Qualifiers

1. .524

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

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/clone="IMAGp998K1811607 ; IMAGE:5240969"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

```

ORIGIN

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Query Match          47.0%; Score 467; DB 13; Length 524;
Best Local Similarity 100.0%; Pred. No. 3.6e-87;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      58 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 117

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 177

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 237

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 297

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 357

Qy     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 417

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 477

Qy     421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 467
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACA 524

```

RESULT 5

AA706226

```

LOCUS      AA706226          549 bp      mRNA      linear      EST 12-JAN-1999
DEFINITION ah28a07.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
            1240116 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR

```

NDF04 ;, mRNA sequence.

ACCESSION AA706226

VERSION AA706226.1 GI:2716144

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 549)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Insert Length: 689 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 451.

FEATURES

source Location/Qualifiers

1. .549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1240116"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_parathyroid_tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCCGCACCAATTTTTTTTTTTTTTTTTTTT
TTTTT-3'], double-stranded cDNA was size selected, ligated
to Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT7T3
vector (Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
adenomas was kindly provided by Dr. Stephen Marx, National
Institute of Diabetes and Digestive and Kidney Diseases,
NIH."

ORIGIN

Query Match 40.6%; Score 404; DB 9; Length 549;
Best Local Similarity 98.5%; Pred. No. 5.5e-74;
Matches 407; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
 |||
 Db 15 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 74
 QY 484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
 |||
 Db 75 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 134
 QY 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAAC 603
 |||
 Db 135 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAAC 194
 QY 604 TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC 663
 |||
 Db 195 TCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCC 254
 QY 664 GAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACC 723
 |||
 Db 255 GAGAACATCCTGGGGAAGGACACCGTCCGGAGGCCGGCTTTACGTCAACAGCGTGAGCACC 314
 QY 724 ACCCTGTCATCCTGGTTCGGGGCAGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGC 783
 |||
 Db 315 ACCCTGTCATCCTGGTTCGGGGCAGCCCGGAAGTGCAACGNGACAGCCAAGTCCTATTGC 374
 QY 784 GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 836
 |||
 Db 375 GTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 427

RESULT 6

AI041451

LOCUS AI041451 412 bp mRNA linear EST 28-AUG-1998

DEFINITION ow36c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
 IMAGE:1648898 3' similar to TR:O14511 O14511 NTAK. ;, mRNA
 sequence.

ACCESSION AI041451

VERSION AI041451.1 GI:3280645

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 412)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source

ORIGIN

Qy	426	CACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	485
Db	1	CACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATC	60
Qy	486	GCTGAAGTGTGAGGCAGCAGCCGGTAATCCCAGCCTTCCTACCGTTGGTTC AAGGATGG	545
Db	61	GCTGAAGTGTGAGGCAGCAGCGATAAATCCCAGCCTTCCTACCGTTGGTTC AAGGATGG	120
Qy	546	CAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAACTC	605
Db	121	CAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAACTC	180
Qy	606	ACGACTACAGTTC AACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	665
Db	181	ACGACTACAGTTC AACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGA	240
Qy	666	GAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCAC	725
Db	241	GAACATCCTGGGGAAGGACACCGTACGAGGCCGGCTTTACGTCAACAGCGTGACGACCAC	300
Qy	726	CCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGT	785

Db 301 CCTGTCATCCTGGTCGGGGCACGCCGGGAAGTGCAACGNGACAGCCAAGTCCTATTGCGT 360

Qy 786 CAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 836
 |||

Db 361 CAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 411

RESULT 7

BX529505

LOCUS BX529505 488 bp mRNA linear EST 27-JUN-2003

DEFINITION BX529505 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGp998N017639 ;
 IMAGE:3153984, mRNA sequence.

ACCESSION BX529505

VERSION BX529505.1 GI:32297863

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 488)

AUTHORS Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
 and Korn,B.

TITLE Mouse UnigeneSet - RZPD2

JOURNAL Unpublished (2003)

COMMENT Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998N017639.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)

[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981)

[bin/showLib.pl.cgi/response?libNo=981](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981) Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

SP6, Primer sequence: ATTTAGGTGACACTATAG.

FEATURES

source

Location/Qualifiers

1. .488

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGp998N017639 ; IMAGE:3153984"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

ORIGIN

Query Match 38.3%; Score 381; DB 13; Length 488;
 Best Local Similarity 91.0%; Pred. No. 3.4e-69;
 Matches 405; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy	469	GTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTAC	528
Db	1	GTGGGTGAGAAGCAGTCGCTCAAGTGTGAGGCAGCGGCGGGAACCCCCAGCCTTCCTAT	60
Qy	529	CGTTGGTTCAAGGATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGC	588
Db	61	CGCTGGTTCAAGGATGGCAAGGAACCTCAACCGGAGTCGTGATATTCGCATCAAGTATGGC	120
Qy	589	AACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAG	648
Db	121	AATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAG	180
Qy	649	TATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTC	708
Db	181	TACGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCGTGAGGGGGCCGACTCCATGTC	240
Qy	709	AACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACA	768
Db	241	AACAGCGTGAGCACCCTCTGTCATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACC	300
Qy	769	GCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTC	828
Db	301	GCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTC	360
Qy	829	TCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGA	888
Db	361	TCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGA	420
Qy	889	TTGTACATGCCAGATCCTAAGCAA	913
Db	421	TTGTACATGCCAGATCCTAAGCAA	445

RESULT 8

BF108794

LOCUS BF108794 427 bp mRNA linear EST 20-OCT-2000

DEFINITION 7152g03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:3525292 3' similar to SW:NTAK_HUMAN O14511 NTAK PROTEIN
 ;contains MSR1.t1 MSR1 repetitive element ;, mRNA sequence.

ACCESSION BF108794

VERSION BF108794.1 GI:10938484

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 427)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 396.

FEATURES Location/Qualifiers
 source 1. .427
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3525292"
 /lab_host="DH10B"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and cloneIDs: Soares NbHSF pool 1:
 309384-310919, 323208-325895 Soares Nb2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 36.6%; Score 363.8; DB 10; Length 427;
 Best Local Similarity 91.3%; Pred. No. 1.3e-65;
 Matches 386; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
Db	5	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCGATCCCGGGGAGAA	64
Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	65	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	124
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	125	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	184
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	185	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	244
Qy	603	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	245	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	304
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722

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|||||
Db      305 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 364
Qy      723 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
|||||
Db      365 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 424
Qy      783 CGT 785
      |||
Db      425 CGT 427

```

RESULT 9

BI410828/c

LOCUS BI410828 949 bp mRNA linear EST 14-AUG-2001

DEFINITION 602963734F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119065 5', mRNA sequence.

ACCESSION BI410828

VERSION BI410828.1 GI:15171751

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 949)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11290 row: d column: 10

High quality sequence start: 28

High quality sequence stop: 919.

FEATURES

source

Location/Qualifiers

1. .949

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:5119065"

/tissue_type="pooled lung tumors"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NCI_CGAP_Lu33"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGAGCGCCGCCTCTGTTTTTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 31.9%; Score 317.4; DB 12; Length 949;
 Best Local Similarity 84.2%; Pred. No. 9e-56;
 Matches 442; Conservative 0; Mismatches 71; Indels 12; Gaps 7;

```

Qy      397 GTGGGCAAGATCCTGTGCACTGACTGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGC 456
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      947 GTGGGCCAGATCCTGGGCACTG-CTGCGCCACCCGCCCAA-CTGAAGAAGATGAAGA-C 891

Qy      457 CAGACGGGACAGGTGGGTGAGAAGCAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCC 516
          || || || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      890 CAAACCAGAAGAGTCGGTGAGAACAGTTTCGCTCAAGTGTGAGGCACGGCCGGGGAAACCC 831

Qy      517 CAGCCTTCCTACC-----GTTGGTTCAAGGATGGC-AAGGAGCTCAACCGCAGCCGAGAC 570
          || | ||| || | ||||| ||||| ||||| ||||| ||||| |||||
Db      830 CCCCACCCCTCCCTATCGCTGGTTTCAAGGATGGCAAAGGAAGTCAACCGGAGTCGTGAT 771

Qy      571 ATTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAG 630
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      770 ATTCGCATCAAGTATGCCAATGGCAGAAAGAACTCACGGCTACAGTTCAACAAAAGTGAG 711

Qy      631 GT--GGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCG 688
          || | | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      710 GTTGGAGGATTGCCGGGGAGTACGTCTGTGAGGCCGAGAACATCCTTGGGGAAGGACACCG 651

Qy      689 TCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGCAGC 748
          | ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      650 TGA-GGGCCGACTCCATGTCAACAGCGTGAGCACCCTCTGTCATCCTGGTCGGGACATG 592

Qy      749 CCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACA 808
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      591 CCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACA 532

Qy      809 TCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGTT 868
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      531 TCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTT 472

Qy      869 TGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAA 913
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      471 TGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAA 427
  
```

RESULT 10

BI651936

LOCUS BI651936 795 bp mRNA linear EST 12-SEP-2001
 DEFINITION 603298677F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5339251 5', mRNA sequence.
 ACCESSION BI651936
 VERSION BI651936.1 GI:15566172
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 795)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM11861 row: j column: 20

High quality sequence stop: 795.

FEATURES Location/Qualifiers

source 1. .795

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5339251"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

ORIGIN

Query Match 27.4%; Score 272.6; DB 12; Length 795;

Best Local Similarity 92.3%; Pred. No. 1.9e-46;

Matches 298; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

```

Qy      592 GGCAGAAAGAACTCACGAC-TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTA 650
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1   GGCAGAAAGAACTCACGGCTTACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTA 60

Qy      651 TGTCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAA 710
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  CGTCTGTGAGGCCGAGAACATCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAA 120

Qy      711 CAGCGTGAGCACCACCCTGTGCATCCTGGTGGGGACGCCCCGGAAGTGCAACGAGACAGC 770
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 CAGCGTGAGCACCCTGTGCATCCTGGTGGGACATGCCCGGAAGTGCAATGAGACCGC 180

Qy      771 CAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTC 830
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 CAAGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTC 240

Qy      831 CTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATT 890

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|||||
Db      241 CTGCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATT 300
QY      891 GTACATGCCAGATCCTAAGCAAA 913
|||||
Db      301 GTACATGCCAGATCCTAAGCAAA 323

```

RESULT 11
BE983573

LOCUS BE983573 333 bp mRNA linear EST 29-APR-2002
DEFINITION UI-M-CG0p-bgi-c-07-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
UI-M-CG0p-bgi-c-07-0-UI 3', mRNA sequence.

ACCESSION BE983573

VERSION BE983573.1 GI:10654893

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 333)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine The following repetitive
elements were found in this cDNA sequence: 15-105,

>GC_rich#Low_complexity

Seq primer: M13 Forward

POLYA=No.

FEATURES

source

Location/Qualifiers

1. .333

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-CG0p-bgi-c-07-0-UI"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NIH_BMAP_Ret4_S2"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine

TAG SEQ=None found"

Query Match 23.6%; Score 234.4; DB 10; Length 333;
Best Local Similarity 95.6%; Pred. No. 1.3e-38;
Matches 241; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

RESULT 12

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LOCUS      AW476657                529 bp      mRNA      linear      EST 24-FEB-2000
DEFINITION uq79e01.y1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:2937336 5'
            similar to TR:O35073 O35073 NTAK ALPHA2-1P ;; mRNA sequence.
ACCESSION  AW476657
VERSION    AW476657.1   GI:7046763
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 529)
  AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL  Unpublished (1997)
COMMENT    Other_ESTs: uq79e01.x1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.

```


cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

MGI:1049756

Seq primer: -40RP from Gibco

High quality sequence stop: 459.

FEATURES

source

Location/Qualifiers

1. .529

/organism="Mus musculus"

/mol_type="mRNA"

/strain="Czech II"

/db_xref="taxon:10090"

/clone="IMAGE:2937336"

/tissue_type="pooled lung tumors"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NCI_CGAP_Lu33"

/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCTCTGTTTTTTTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 23.4%; Score 232.2; DB 10; Length 529;

Best Local Similarity 93.1%; Pred. No. 4.6e-38;

Matches 243; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy	653	TCTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACA	712
Db	2	TCTGTGAGGCCGAGAACATCCTTGGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACA	61
Qy	713	GCGTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCA	772
Db	62	GCGTGAGCACCCTGTCATCCTGGTCGGGACATGCCCGGAAGTGAATGAGACCGCCA	121
Qy	773	AGTCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCT	832
Db	122	AGTCCTACTGTGTGAATGGAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCT	181
Qy	833	GCAAATGTCCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGT	892
Db	182	GCAAATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGT	241
Qy	893	ACATGCCAGATCCTAAGCAAA	913
Db	242	ACATGCCAGATCCTAAGCAAA	262

RESULT 13
 AA772412
 LOCUS AA772412 297 bp mRNA linear EST 31-DEC-1998
 DEFINITION ai44e12.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
 1359886 3' similar to TR:P43328 P43328 NEU DIFFERENTIATION FACTOR
 NDF04 ;, mRNA sequence.
 ACCESSION AA772412
 VERSION AA772412.1 GI:2824195
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 297)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

 Possible reversed clone: similarity on wrong strand
 Possible reversed clone: polyT not found
 Insert Length: 667 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 267.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="1359886"
 /tissue_type="parathyroid tumor"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_parathyroid_tumor_NbHPA"
 /note="Organ: parathyroid gland; Vector: pT7T3D
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTT
 TTTT-3'], double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,

ORIGIN

[illegible]

COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998M133119.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
[http://www.rzpd.de/CloneCards/cgi-](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972)
[bin/showLib.pl.cgi/response?libNo=972](http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972) Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers
 source 1. .362
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGp998M133119 ; IMAGE:1240116"
 /tissue_type="parathyroid tumor"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_parathyroid_tumor_NbHPA"
 /note="Organ: parathyroid gland; Vector: pT7T3D
 (Pharmacia) with a modified polylinker; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTT
 TTTT-3'], double-stranded cDNA was size selected, ligated
 to Eco RI adapters (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT7T3
 vector (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid
 adenomas was kindly provided by Dr. Stephen Marx, National
 Institute of Diabetes and Digestive and Kidney Diseases,
 NIH."

ORIGIN

Query Match 18.1%; Score 180; DB 13; Length 362;
Best Local Similarity 99.4%; Pred. No. 3.2e-27;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	656	GCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCG	715
Db	362	GCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGNCCGGCTTTACGTCAACAGCG	303
Qy	716	TGAGCACCACCCTGTCTATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGT	775
Db	302	TGAGCACCACCCTGTCTATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGT	243
Qy	776	CCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCA	835
Db	242	CCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCA	183
Qy	836	A	836
Db	182	A	182

RESULT 15

AW762061

LOCUS AW762061 256 bp mRNA linear EST 04-MAY-2000
DEFINITION ur53c01.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3153984 5'
 similar to TR:O35073 O35073 NTAK ALPHA2-1P ;; mRNA sequence.
ACCESSION AW762061

```

VERSION      AW762061.1   GI:7693978
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 256)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE        National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Other_ESTs: ur53c01.x1
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              image.llnl.gov/image/html/iresources.shtml

```

ORIGIN

Qy	723	CACCCTGTCATCCTGGTCGGGGCACGCCC	GGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db	1	CACTCTGTCATCCTGGTCGGGACATGCCC	GGAAGTGCAATGAGACCGCCAAGTCCTACTG	60
Qy	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGG	CATCAACCAGCTCTCCTGCAAATGTCC	842
Db	61	TGTGAATGGAGGCGTGTGCTACTACATCGAGGG	CATCAACCAGCTCTCCTGCAAATGTGC	120
Qy	843	AAATGGATTCTTCGGACAGAGATGTTTGGAGAA	ACTGCCTTTGCGATTGTACATGCCAGA	902

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      ||| |||||
Db      121 AACGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCTGA 180
Qy      903 TCCTAAGCAAA 913
      |||||
Db      181 TCCTAAGCAAA 191

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Search completed: August 15, 2004, 09:42:28
Job time : 3164.99 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 02:48:13 ; Search time 4242.5 Seconds
(without alignments)
10155.083 Million cell updates/sec

Title: US-09-864-675-1
Perfect score: 994
Sequence: 1 atgaggcgcgacccggcccc.....caccttggatttgaattaaa 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
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27: em_sts:*

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 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
	1	992.4	99.8	2613	9	AK124504	AK124504 Homo sapi
	2	913.2	91.9	3020	9	AB005060	AB005060 Homo sapi
	3	900	90.5	1884	6	AR098145	AR098145 Sequence
	4	900	90.5	1884	6	AR116617	AR116617 Sequence
	5	881	88.6	993	6	AR072053	AR072053 Sequence
	6	800	80.5	2947	10	D89995	D89995 Rattus sp.
	7	799.4	80.4	3076	6	E16456	E16456 Rat mRNA fo
	8	799.4	80.4	3077	10	D89996	D89996 Rattus sp.
	9	738.6	74.3	3441	6	AR072052	AR072052 Sequence
	10	547.2	55.1	1607	6	AR098144	AR098144 Sequence
	11	547.2	55.1	1607	6	AR116616	AR116616 Sequence
	12	492	49.5	1476	6	AR098146	AR098146 Sequence
	13	492	49.5	1476	6	AR116618	AR116618 Sequence
	14	492	49.5	2268	6	AR098155	AR098155 Sequence
	15	492	49.5	2268	6	AR116627	AR116627 Sequence
	16	487.4	49.0	2188	10	AB001576	AB001576 Rattus sp
	17	467.8	47.1	2467	6	AR098143	AR098143 Sequence
	18	467.8	47.1	2467	6	AR116615	AR116615 Sequence
	19	424.8	42.7	118504	9	AC094080	AC094080 Homo sapi
c	20	424.8	42.7	152838	2	AC011589	AC011589 Homo sapi
	21	424.8	42.7	170797	9	AC011379	AC011379 Homo sapi
	22	424.8	42.7	210675	2	AC026272	AC026272 Homo sapi
	23	424	42.7	1054	6	AX406616	AX406616 Sequence
	24	424	42.7	1054	9	HS2NRG01	AF119151 Homo sapi
	25	387.2	39.0	139074	2	AC131191	AC131191 Mus muscu
	26	384	38.6	253462	2	AC096477	AC096477 Rattus no
	27	359.6	36.2	1207	6	AR072054	AR072054 Sequence
	28	227.2	22.9	240	10	AY227025	AY227025 Mus muscu
	29	173	17.4	419	6	AX406617	AX406617 Sequence
	30	173	17.4	419	9	HS2NRG02	AF119152 Homo sapi
	31	173	17.4	120236	9	AC008523	AC008523 Homo sapi
c	32	173	17.4	189049	9	AC008667	AC008667 Homo sapi
	33	142.6	14.3	85703	2	AC020830	AC020830 Mus muscu

	34	142.6	14.3	190228	10	AC127350	AC127350 Mus muscu
	35	139.4	14.0	226038	2	AC106592	AC106592 Rattus no
	36	139.4	14.0	273080	2	AC098540	AC098540 Rattus no
c	37	139.4	14.0	302176	2	AC096479	AC096479 Rattus no
	38	135.6	13.6	142	6	AR072064	AR072064 Sequence
	39	124.6	12.5	493	6	AX406618	AX406618 Sequence
	40	124.6	12.5	493	9	HS2NRG03	AF119153 Homo sapi
	41	122.4	12.3	350	6	AX406619	AX406619 Sequence
	42	122.4	12.3	350	9	HS2NRG04	AF119154 Homo sapi
c	43	108.4	10.9	205280	2	BX323592	BX323592 Danio rer
	44	108.4	10.9	207840	5	BX005008	BX005008 Zebrafish
c	45	108	10.9	85703	2	AC020830	AC020830 Mus muscu

ALIGNMENTS

RESULT 1

AK124504

LOCUS AK124504 2613 bp mRNA linear PRI 09-SEP-2003

DEFINITION Homo sapiens cDNA FLJ42513 fis, clone BRACE2046295, highly similar to NTAK PROTEIN.

ACCESSION AK124504

VERSION AK124504.1 GI:34530302

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kawakami,B., Sugiyama,A., Takemoto,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2613)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

source Location/Qualifiers
1. .2613
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="BRACE2046295"
/tissue_type="cerebellum"
/clone_lib="BRACE2"
/note="cloning vector: pME18SFL3"

ORIGIN

Query Match 99.8%; Score 992.4; DB 9; Length 2613;
Best Local Similarity 99.9%; Pred. No. 6.3e-187;
Matches 993; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 60
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Db     436 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCCTGC 495

Qy     61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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Db     496 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 555

Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db     556 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 615

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Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 735

Qy    301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 795

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 855

Qy    421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 915

Qy    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     916 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 975

Qy    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     976 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 1035

Qy    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1036 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 1095

Qy    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db 1096 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 1155
 Qy 721 ACCACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1156 ACCACCCTGTCATCCTGGTCTGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 1215
 Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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 Db 1216 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1275
 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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 Db 1276 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1335
 Qy 901 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 960
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 Db 1336 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 1395
 Qy 961 TCAACTTCTCCAAGCACCTTGGATTGAATTAAA 994
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 Db 1396 TCAACTTCTCCAAGCACCTTGGATTGAATTAAA 1429

RESULT 2

AB005060

LOCUS AB005060 3020 bp mRNA linear PRI 14-NOV-1997

DEFINITION Homo sapiens mRNA for NTAK, complete cds.

ACCESSION AB005060

VERSION AB005060.1 GI:2626738

KEYWORDS NTAK.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Higashiyama,S., Horikawa,M., Yamada,K., Ichino,N., Nakano,N.,
Nakagawa,T., Miyagawa,J., Matsushita,N., Nagatsu,T., Taniguchi,N.
and Ishiguro,H.

TITLE A novel brain-derived member of the epidermal growth factor family
that interacts with ErbB3 and ErbB4

JOURNAL J. Biochem. 122 (3), 675-680 (1997)

MEDLINE 98006324

PUBMED 9348101

REFERENCE 2 (bases 1 to 3020)

AUTHORS Ishiguro,H.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-1997) Hiroshi Ishiguro, Fujita Health University,
ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan
(E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

FEATURES

source Location/Qualifiers
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 /organism="Homo sapiens"
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 CDS 226. .2778

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ORIGIN

Query Match          91.9%;   Score 913.2;   DB 9;   Length 3020;
Best Local Similarity 99.7%;   Pred. No. 3.4e-171;
Matches 915; Conservative    0; Mismatches    3; Indels        0; Gaps        0;

Qy       1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTCGCTCGCCTGC 60
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Db     502 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTCGCTCGCCTGC 561

Qy       61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
|
Db     562 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 621

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
|
Db     622 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 681

Qy      181 CCCGCCCTCGGGTTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db     682 CCCGCCCTCGGGTTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 741

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
|
Db     742 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 801

Qy      301 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
|
Db     802 CGCTACATCTTTTTCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 861

Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
|
Db     862 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 921

Qy      421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db      922 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 981
Qy      481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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Db      982 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 1041
Qy      541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
        |||
Db      1042 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 1101
Qy      601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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Db      1102 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 1161
Qy      661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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Db      1162 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 1221
Qy      721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Db      1222 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 1281
Qy      781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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Qy      841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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Qy      901 GATCCTAAGCAAAGTGTC 918
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RESULT 3

AR098145

LOCUS AR098145 1884 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 5 from patent US 6074841.

ACCESSION AR098145

VERSION AR098145.1 GI:12807402

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1884)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6074841-A 5 13-JUN-2000;

FEATURES Location/Qualifiers

source 1. .1884

/organism="unknown"

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ORIGIN

Query Match 90.5%; Score 900; DB 6; Length 1884;

Best Local Similarity 99.3%; Pred. No. 1.4e-168;

Matches 914; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	218	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	277
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	278	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	337
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	517
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	816
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
Db	997	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	1056

Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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 Db 1117 GATCCTAAGCAAAAGCACCT 1136

RESULT 4

AR116617

LOCUS AR116617 1884 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 5 from patent US 6133423.

ACCESSION AR116617

VERSION AR116617.1 GI:14096939

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1884)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6133423-A 5 17-OCT-2000;

FEATURES Location/Qualifiers

source 1..1884

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 90.5%; Score 900; DB 6; Length 1884;

Best Local Similarity 99.3%; Pred. No. 1.4e-168;

Matches 914; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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 Db 218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277
 Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
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 Db 278 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337
 Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||
 Db 338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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 Db 398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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 Db 458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
 Qy 301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 518 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577

Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636

Qy 421 TCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Db 637 TCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 696

Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 697 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756

Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
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 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 816

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876

Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936

Qy 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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Qy 901 GATCCTAAGCAAAGTGTCT 920
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 Db 1117 GATCCTAAGCAAAGCACCT 1136

RESULT 5

AR072053

LOCUS AR072053 993 bp DNA linear PAT 18-FEB-2000

DEFINITION Sequence 3 from patent US 5912326.

ACCESSION AR072053

VERSION AR072053.1 GI:7222941

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 993)

AUTHORS Chang,H.

TITLE Cerebellum-derived growth factors

JOURNAL Patent: US 5912326-A 3 15-JUN-1999;

FEATURES Location/Qualifiers


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Query Match 88.6%; Score 881; DB 6; Length 993;
Best Local Similarity 93.0%; Pred. No. 8.5e-165;
Matches 923; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
Db 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 60

Qy 61 TACTCGCCCGAGCCTCAAGTCAGTGAGGACAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
Db 61 TACTCGCCCGAGCCTCAAGTCCGTGCAGGACAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
Db 121 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCAGCTCTAACAGCACCCGAGAGCCT 180

Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
Db 181 CCCGCCTCGGGTCGGGTGGCGTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
Db 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 300

Qy 301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
Db 301 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 360

Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
Db 361 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
Db 421 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 480

Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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Db 541 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG 600

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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ORIGIN

Query Match 80.5%; Score 800; DB 10; Length 2947;
 Best Local Similarity 91.8%; Pred. No. 1e-148;
 Matches 845; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTGCTCGCCTGC	60
Db	403	ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	462
Qy	61	TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	463	TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	522
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	523	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	582
Qy	181	CCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	583	CCCGCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	642
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	643	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCAGCGCCGCTCGAAAGGAACCAG	702
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	703	CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC	762
Qy	361	CCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	763	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	822
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	823	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	882

Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 883 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 942
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
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 Db 943 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG 1002
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 1003 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 1062
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTACGTCAACAGCGTGAGC 720
 || ||||||| ||||||||| || || ||||||| ||||||| ||||||| |||||||
 Db 1063 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 1122
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTTAT 780
 ||||| ||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
 Db 1123 ACCACTCTGTCGTCCTGGTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCTTAC 1182
 Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 || || ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
 Db 1183 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1242
 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
 ||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
 Db 1243 CCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1302
 Qy 901 GATCCTAAGCAAAGTGTCTT 920
 ||||||||| |||||
 Db 1303 GATCCTAAGCAAAGCACCT 1322

RESULT 7

E16456

LOCUS E16456 3076 bp DNA linear PAT 28-JUL-1999

DEFINITION Rat mRNA for neuregulin-like Transmembrane Activator for ErbB Kinases (NTAK).

ACCESSION E16456

VERSION E16456.1 GI:5711139

KEYWORDS JP 1998179166-A/1.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 3076)

AUTHORS Higashiyama,S., Taniguchi,N., Ishiguro,K. and Nagatsu,T.

TITLE GENE ENCODING RECEPTOR TYPE TYROSINE-KINASE ERB B LIGAND AND ITS

JOURNAL Patent: JP 1998179166-A 1 07-JUL-1998;

HIGASHIYAMA SHIGEKI

COMMENT OS Rattus sp. (rat)

PN JP 1998179166-A/1

PD 07-JUL-1998

PF 25-DEC-1996 JP 1996356998

PI HIGASHIYAMA SHIGEKI, TANIGUCHI NAOYUKI, ISHIGURO KEIJI, PI

NAGATSU TOSHIHARU

PC C12N15/09,C07K14/705,C07K16/28,C12N5/10,C12N15/02,C12P21/02,
PC C12P21/08,
PC C12Q1/68,G01N33/53,G01N33/566//A61K31/70,A61K38/46,A61K39/395,
PC A61K48/00,

PC C07H21/04,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91); CC

strandedness: Double;

CC topology: Linear;

FH Key Location/Qualifiers

FH

FT source 1. .3076

FT /organism='Rattus sp.'

FT /cell_line='PC12'

FT CDS 232. .2814

FT /product='NTAK protein'.

FEATURES Location/Qualifiers
source 1. .3076
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

ORIGIN

Query Match 80.4%; Score 799.4; DB 6; Length 3076;
Best Local Similarity 92.2%; Pred. No. 1.3e-148;
Matches 842; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTGCTCGCCTGC 60
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Db      556 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 615

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          |||
Db      616 TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
          |||
Db      676 GGCAAGGTACAGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 735

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
          |||
Db      736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 795

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db      796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855

Qy      301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db      856 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 915

Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          |||
Db      916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975

Qy      421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db      976 TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1035
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Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 1036 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCAGCCCTCCTATCGATGGTTCAAG 1095

Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG 600
 || ||||| ||||| || || ||||| ||||| ||||| |||||
 Db 1096 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTGCGATCAAGTATGGCAACGGCAGAAAG 1155

Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1156 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 1215

Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 || ||||| ||||| ||||| || ||||| || ||||| |||||
 Db 1216 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 1275

Qy 721 ACCACCCTGTGCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1276 ACCACTCTGTGTCCTGGTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 1335

Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1336 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1395

Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1396 CCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1455

Qy 901 GATCCTAAGCAAA 913
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 Db 1456 GATCCTAAGCAAA 1468

RESULT 8

D89996

LOCUS D89996 3077 bp mRNA linear ROD 07-FEB-1999
 DEFINITION Rattus sp. mRNA for NTAK alpha2, complete cds.
 ACCESSION D89996
 VERSION D89996.1 GI:2605631
 KEYWORDS NTAK alpha2.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (sites)
 AUTHORS Higashiyama,S., Horikawa,M., Yamada,K., Ichino,N., Nakano,N.,
 Nakagawa,T., Miyagawa,J., Matsushita,N., Nagatsu,T., Taniguchi,N.
 and Ishiguro,H.
 TITLE A novel brain-derived member of the epidermal growth factor family
 that interacts with ErbB3 and ErbB4
 JOURNAL J. Biochem. 122 (3), 675-680 (1997)
 MEDLINE 98006324
 PUBMED 9348101
 REFERENCE 2 (bases 1 to 3077)
 AUTHORS Ishiguro,H.

TITLE Direct Submission
JOURNAL Submitted (21-DEC-1996) Hiroshi Ishiguro, Fujita Health University,
ICMS; 1-98, kutsukake-cho, Toyoake, Aichi 470-11, Japan
(E-mail:hishi@fujita-hu.ac.jp, Tel:0562-93-9393, Fax:0562-93-8831)

FEATURES Location/Qualifiers
source 1. .3077
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/cell_line="PC12"
/cell_type="pheochromocytoma"
CDS 233. .2815
/codon_start=1
/product="NTAK alpha2"
/protein_id="BAA23345.1"
/db_xref="GI:2605632"
/translation="MRQVCCSALPPPLEKARCSSYSYSDSSSSSSSSNNSSSSTSSRSS
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SSNSTREPPASGRVALVKVLDKWPLRSGGLQREQVISVGCAPLERNQRYIFFLEPTE
QPLVFKTAFAPVDPNGKNIKKEVGKILCTDCATRPKLKMKSQTEVGEKQSLKCEAA
AGNPQPSYRWFKDGEKELNRSRDIRIKYNGRKNRSLQFNKVKVEDAGEYVCEAENILG
KDTVGRHLHVNVSSTTLSSWSGHARKCNETAKSYCVNGGVCYYIEGINQLSCKCPNGF
FGQRCLEKLPLRLYMPDPKQKAEELYQKRVLTITGICVALLVVGIVCVVAYCKTKKQR
RQMHHHLRQNMCPAHQNRSLANGPSHPRLDPEEIQMADYISKNPATDHVIRREAETT
FSGSHSCSPSHHCSTATPTSSHRHESHTWSLSESLTSDSQSGIMLSSVGTSKCNSP
ACVEARARRAAAYSQEERRRAAMPPYHDSIDSLRDSPHSERYVSALTTPARLSPVDFH
YSLATQVPTFEITSPNSAHAVSLPPAAPISYRLAEQQPLL RHPAPPGP GPGADMQR
SYDSYYYPAAGPGPRRGACALGGSLSLSPASPFRIPEDEYETTQECAPPPPPRPRTR
GASRRTSAGPRRWRRSRLNGLAAQRARAARDSLSLSGSGCGSASASDDDADDADGAL
AAESTPFLGLRAAHDALRSDSPPLCPAADSRTYYSLDSHSTRASSRHSRGPPTRAKQD
SGPL"

ORIGIN

Query Match 80.4%; Score 799.4; DB 10; Length 3077;
Best Local Similarity 92.2%; Pred. No. 1.3e-148;
Matches 842; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	557	ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC	616
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	617	TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	676
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	677	GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT	736
Qy	181	CCCGCCTCGGGTTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	737	CCCGCCTCGGGTTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	796
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	797	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG	856

Qy 301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 857 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 916
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 || |||
 Db 917 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 976
 Qy 421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 ||| |||
 Db 977 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1036
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 || |||
 Db 1037 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 1096
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAAG 600
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 Db 1097 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAAG 1156
 Qy 601 AACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Db 1157 AACTCAGGCTACAGTTCAACAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 1216
 Qy 661 GCCGAGAACATCCTGGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 1217 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGGCCGGCTCCATGTCAACAGTGTGAGC 1276
 Qy 721 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 ||| |||
 Db 1277 ACCACTCTGTCGTCTGGTTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 1336
 Qy 781 TGCCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 || |||
 Db 1337 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1396
 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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 Db 1397 CCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1456
 Qy 901 GATCCTAAGCAAA 913
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 Db 1457 GATCCTAAGCAAA 1469

RESULT 9

AR072052

LOCUS AR072052 3441 bp DNA linear PAT 18-FEB-2000

DEFINITION Sequence 1 from patent US 5912326.

ACCESSION AR072052

VERSION AR072052.1 GI:7222940

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 3441)

AUTHORS Chang, H.
TITLE Cerebellum-derived growth factors
JOURNAL Patent: US 5912326-A 1 15-JUN-1999;
FEATURES Location/Qualifiers
source 1. .3441
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 74.3%; Score 738.6; DB 6; Length 3441;
Best Local Similarity 90.4%; Pred. No. 1.6e-136;
Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
          |||
Db     180 ATGAGGCGCGACCCGGCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          |||
Db     240 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
          |||
Db     300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 359

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
          |||
Db     360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db     420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479

Qy     301 CGCTACATCTTTTTCTGGAGCCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
          |||
Db     480 CGCTACATCTTTTTCTGGAGCCCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 539

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
          ||
Db     540 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 599

Qy     421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
          |||
Db     600 TGCGCAACCCGGCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 659

Qy     481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
          ||
Db     660 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCAAGCCTCCTATCGATGGTTCAAG 719

Qy     541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 600
          ||
Db     720 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAAG 779

Qy     601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
          |||
Db     780 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 839
```


Qy 611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
 |||||
 Db 242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301
 Qy 671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
 |||||
 Db 302 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCACCTCTGT 361
 Qy 731 CATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
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 Db 362 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421
 Qy 791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGAT 850
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 Db 422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 481
 Qy 851 TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC 910
 |||||
 Db 482 TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC 541
 Qy 911 AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC 970
 |||||
 Db 542 AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC 601
 Qy 971 CAAGCACCTTGGATTTGAATTAAA 994
 |||||
 Db 602 CAAGCACCTTGGATTTGAATTGAA 625

RESULT 11

AR116616

LOCUS AR116616 1607 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 3 from patent US 6133423.

ACCESSION AR116616

VERSION AR116616.1 GI:14096938

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1607)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6133423-A 3 17-OCT-2000;

FEATURES Location/Qualifiers

source 1. .1607

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 55.1%; Score 547.2; DB 6; Length 1607;

Best Local Similarity 92.3%; Pred. No. 1.6e-98;

Matches 576; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430

Db 2 CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 49.5%; Score 492; DB 6; Length 1476;
Best Local Similarity 92.8%; Pred. No. 1.5e-87;
Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | || | | | | || | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
      |||||
Db      458 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
      |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy      843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 902
      |||||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 637

Qy      903 TCCTAAGCAAAGTGTC 918
      |||||
Db      638 TCCTAAGCAAAAAGCC 653
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RESULT 13

AR116618

LOCUS AR116618 1476 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 7 from patent US 6133423.

ACCESSION AR116618

VERSION AR116618.1 GI:14096940

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 1476)
 AUTHORS Gearing,D.P. and Busfield,S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6133423-A 7 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1. .1476
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 49.5%; Score 492; DB 6; Length 1476;
 Best Local Similarity 92.8%; Pred. No. 1.5e-87;
 Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
Db	98	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA	157
Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723	CACCCGTGTCATCCTGGTCCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG	782
Db	458	CACCCGTGTCATCCTGGTCCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG	517
Qy	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC	842
Db	518	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC	577
Qy	843	AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA	902
Db	578	AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA	637
Qy	903	TCCTAAGCAAAGTGTC	918
Db	638	TCCTAAGCAAAAAGCC	653

RESULT 14
 AR098155
 LOCUS AR098155 2268 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 31 from patent US 6074841.
 ACCESSION AR098155
 VERSION AR098155.1 GI:12807412
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 2268)
 AUTHORS Gearing,D.P. and Busfield,S.J.
 TITLE Don-1 gene and polypeptides and uses therefor
 JOURNAL Patent: US 6074841-A 31 13-JUN-2000;
 FEATURES Location/Qualifiers
 source 1. .2268
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 49.5%; Score 492; DB 6; Length 2268;
 Best Local Similarity 92.8%; Pred. No. 1.5e-87;
 Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
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Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457
Qy	723	CACCCTGTCATCCTGGTCGGGGCACGCCCCGAAGTGCAACGAGACAGCCAAGTCCTATTG	782
Db	458	CACCCTGTCATCCTGGTCGGGGCACGCCCCGAAGTGCAACGAGACAGCCAAGTCCTATTG	517
Qy	783	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC	842
Db	518	CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC	577
Qy	843	AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA	902

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      903 TCCTAAGCAAAGTGTC 918
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RESULT 15

AR116627

LOCUS AR116627 2268 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 31 from patent US 6133423.

ACCESSION AR116627

VERSION AR116627.1 GI:14096949

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2268)

AUTHORS Gearing,D.P. and Busfield,S.J.

TITLE Don-1 gene and polypeptides and uses therefor

JOURNAL Patent: US 6133423-A 31 17-OCT-2000;

FEATURES Location/Qualifiers

source 1. .2268

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 49.5%; Score 492; DB 6; Length 2268;

Best Local Similarity 92.8%; Pred. No. 1.5e-87;

Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy      363 CCTCGATACCAACGGCAAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
          || || | || | | | | || | || | || | || | ||
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
          |||||||||||||||||||||||||||||||||||||||||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
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Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
          |||||||||||||||||||||||||||||||||||||||||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

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Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
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Db	458		CACCCTGTCATCCTGGTCGGGGGCACGCCC	CGGAAGTGCAACGAGACAGCCAAGTCCTATTG	517
Qy	783		CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC		842
Db	518		CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC		577
Qy	843		AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA		902
Db	578		AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA		637
Qy	903		TCCTAAGCAAAGTGTC		918
Db	638		TCCTAAGCAAAAAGCC		653

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Job time : 4249.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 02:37:58 ; Search time 476.763 Seconds
(without alignments)
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Title: US-09-864-675-1
Perfect score: 994
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
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2	900	90.5	1884	2	AAV17814	Aav17814 Homo sapi
3	882	88.7	1803	2	AAT87923	Aat87923 Rat cereb
4	849	85.4	897	6	AAS18020	Aas18020 Human cDN
5	799.4	80.4	3076	2	AAV43674	Aav43674 Receptor
6	788	79.3	1863	7	ABS56035	Abs56035 cDNA enco
7	738.6	74.3	3441	2	AAT87922	Aat87922 Rat cereb

8	547.2	55.1	1607	2	AAV17813	Aav17813	Mus muscu
9	535.2	53.8	1561	7	ABS56034	Abs56034	cDNA enco
10	492	49.5	2268	2	AAV17816	Aav17816	Homo sapi
11	491	49.4	1474	7	ABS56036	Abs56036	cDNA enco
12	491	49.4	2266	7	ABS56045	Abs56045	cDNA enco
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16	424	42.7	1054	6	ABL40993	Abl40993	Human neu
17	380	38.2	667	2	AAT87924	Aat87924	Human cer
18	173	17.4	419	6	ABL40994	Abl40994	Human neu
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20	124.6	12.5	480	6	ABL40995	Abl40995	Human neu
21	122.4	12.3	350	6	ABL40996	Abl40996	Human neu
22	95.4	9.6	1140	2	AAQ62840	Aaq62840	GGF2BPP2.
23	95.4	9.6	1140	2	AAQ58321	Aaq58321	GGF2BPP2.
24	95.4	9.6	1140	2	AAQ74912	Aaq74912	Bovine gl
25	95.4	9.6	1140	2	AAT31001	Aat31001	Glial gro
26	95.4	9.6	1140	2	AAT48088	Aat48088	Human neu
27	95.4	9.6	1140	2	AAT06731	Aat06731	BPP2 glia
28	95.4	9.6	1140	2	AAX81201	Aax81201	Nucleotid
29	91.8	9.2	1193	2	AAQ30670	Aaq30670	GGF2BPP2.
30	91.8	9.2	1193	2	AAQ62849	Aaq62849	GGF-II cD
31	91.8	9.2	1193	2	AAQ58303	Aaq58303	GGF-II cD
32	91.8	9.2	1193	2	AAQ74885	Aaq74885	Putative
33	91.8	9.2	1193	2	AAT30997	Aat30997	Bovine gl
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36	87	8.8	300	6	ABL40997	Abl40997	Human neu
37	79	7.9	1986	2	AAZ32061	Aaz32061	Human MET
38	78.2	7.9	1027	5	AAF80062	Aaf80062	Nucleotid
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41	77.4	7.8	2003	2	AAT30995	Aat30995	Glial gro
42	77.4	7.8	2003	2	AAT48090	Aat48090	Human neu
43	77.4	7.8	2003	2	AAT06739	Aat06739	Glial gro
44	77.4	7.8	2003	2	AAZ32062	Aaz32062	Human MET
45	77.4	7.8	2003	5	AAC90319	Aac90319	I36352 cD

ALIGNMENTS

RESULT 1

AAS18019

ID AAS18019 standard; cDNA; 994 BP.

XX

AC AAS18019;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2alpha, NRG-2alpha.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;

KW cell survival; cell growth; cell differentiation; erbB receptor;

KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;

KW atherosclerosis; vascular lesion; vascular hypertension;

KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .993
 FT /*tag= a
 FT /product= "NRG-2alpha"
 XX
 PN WO200189568-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016896.
 XX
 PR 23-MAY-2000; 2000US-0206495P.
 XX
 PA (CENE-) CENES PHARM INC.
 XX
 PI Marchionni MA;
 XX
 DR WPI; 2002-097612/13.
 DR P-PSDB; AAU11635.
 XX
 PT Neuregulin-2 polypeptide and polynucleotide useful for treating multiple
 PT sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's disease, by
 PT increasing mitogenesis, survival, growth or differentiation of a cell.
 XX
 PS Claim 57; Fig 6; 79pp; English.
 XX
 CC The invention relates to a substantially pure neuregulin (NRG)-2
 CC polypeptide comprising or consisting of a sequence for human NRG-2alpha
 CC or NRG-2beta (clone 2b7) and the polynucleotides encoding the. Also
 CC included are a vector expressing the protein, a host cell comprising the
 CC vector, a transgenic non-human animal transformed with the vector or
 CC having a knockout mutation in one or both NRG-2 alleles and an anti-NRG-2
 CC antibody. Analysis of mutations in NRG-2 in an individual is useful for
 CC diagnosing an increased likelihood of developing a NRG-2-related disease
 CC or condition in a test subject. NRG-2 is useful for increasing the
 CC mitogenesis, survival, growth or differentiation of a cell (e.g. a
 CC neuronal cell), where the cell expresses an erbB receptor. NRG-2 is
 CC useful for treating diseases and disorders such as cardiomyopathy
 CC (preferably degenerative congenital disease), ischaemic damage, cardiac
 CC trauma or heart failure or which has a condition affecting smooth muscle
 CC which include atherosclerosis, vascular lesion, vascular hypertension,
 CC and degenerative congenital vascular disease, myasthenia gravis, a
 CC neurodegenerative disorder, peripheral neuropathy, a sensory nerve fiber
 CC neuropathy, a motor fiber and a sensory nerve fiber neuropathy, multiple
 CC sclerosis, amyotrophic lateral sclerosis, spinal muscular atrophy, nerve
 CC injury, Alzheimer's disease, Parkinson's disease, cerebellar ataxia, and
 CC spinal cord injury. The antibody is useful for treatment of a tumour

CC comprising inhibiting proliferation of a tumour cell preferably a glial
CC tumour cell, for treating of neurofibromatosis by inhibiting glial cell
CC mitogenesis. The present sequence encodes NRG-2alpha

XX

SQ Sequence 994 BP; 230 A; 279 C; 304 G; 181 T; 0 U; 0 Other;

Query Match 100.0%; Score 994; DB 6; Length 994;

Best Local Similarity 100.0%; Pred. No. 4.8e-230;

Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60

Qy     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180

Qy    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        |||
Db    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300

Qy    301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||
Db    301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
        |||
Db    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

Qy    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
        |||
Db    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480

Qy    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
        |||
Db    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540

Qy    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
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Qy    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
        |||
Db    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660

Qy    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
        |||
Db    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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Qy 721 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 721 ACCACCCTGTCATCCTGGTCGGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780

Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 |||
 Db 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840

Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
 |||
 Db 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900

Qy 901 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 960
 |||
 Db 901 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 960

Qy 961 TCAACTTCTCCAAGCACCTTGGATTTGAATTAAA 994
 |||
 Db 961 TCAACTTCTCCAAGCACCTTGGATTTGAATTAAA 994

RESULT 2

AAV17814

ID AAV17814 standard; cDNA; 1884 BP.

XX

AC AAV17814;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;
 KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
 KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
 KW wound healing; transmembrane; ss.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	664..1884
FT		/*tag= a
FT		/note= "don-1 polypeptide"

XX

PN W09807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US014585.

XX

PR 19-AUG-1996; 96US-00699591.

PR 19-NOV-1996; 96US-00753007.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 1998-169084/15.
 DR P-PSDB; AAW48381.
 XX
 PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.
 XX
 PS Claim 4; Fig 3; 121pp; English.
 XX
 CC The sequence is that of a human don-1 gene splice variant. Don-1
 CC polypeptides stimulate proliferation of epithelial cells and thus are
 CC implicated in melanomas and adenocarcinomas in which epithelial cells
 CC proliferate out of control. Compounds that interfere with don-1 mediated
 CC cell proliferation can be used in the treatment of tumours such as
 CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
 CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
 CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
 CC cell proliferation, e.g. for wound healing
 XX
 SQ Sequence 1884 BP; 426 A; 607 C; 560 G; 291 T; 0 U; 0 Other;

Query Match 90.5%; Score 900; DB 2; Length 1884;
 Best Local Similarity 99.3%; Pred. No. 2.8e-207;
 Matches 914; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
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Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	278	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	337
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	338	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	397
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	398	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	457
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG	300
Db	458	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG	517
Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	518	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	577
Qy	361	CCCCTCGATACCAACGGCAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	578	CCCCT-GATACCAACGGCAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC	636
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	637	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	696
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540

Db	697	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	756
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	757	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	816
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	817	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	876
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	877	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	936
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	937	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	996
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
Db	997	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	1056
Qy	841	CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA	900
Db	1057	CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA	1116
Qy	901	GATCCTAAGCAAAGTGTCTCT	920
Db	1117	GATCCTAAGCAAAAGCACCT	1136

RESULT 3

AAT87923

ID AAT87923 standard; cDNA; 1803 BP.

XX

AC AAT87923;

XX

DT 18-DEC-1997 (first entry)

XX

DE Rat cerebellum derived growth factor 2 cDNA.

XX

KW Rat; cerebellum derived growth factor; CDGF2; screening; binding;

KW modulation; erbB type receptor; identification; indication; risk;

KW proliferation; differentiation; induction; neuron; hyperplasia;

KW stem cell culture; intracerebral graft; alleviation; repair;

KW behavioural defect; nervous system; central; peripheral; nerve;

KW prosthesis; damage; entubulation; cell survival; treatment; injury;

KW trauma; ischaemia; ischemia; stroke; infection; disorder; inflammation;

KW neurodegeneration; disease; Parkinson's; Huntingdon's;

KW amyotrophic lateral sclerosis; sensory; retina;

KW spinocerebellar degeneration; multiple sclerosis; neoplasia;

KW amalignant glioma; medulloblastoma; neuroectodermal tumour; ds.

XX

OS Rattus rattus.

XX

FH Key Location/Qualifiers

FT CDS 1. .993
 FT /*tag= a
 FT sig_peptide 1. .69
 FT /*tag= b
 FT mat_peptide 70. .990
 FT /*tag= c
 FT /product= "cerebellum_derived_growth_factor"
 XX
 PN WO9709425-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 09-SEP-1996; 96WO-US014484.
 XX
 PR 08-SEP-1995; 95US-00525864.
 XX
 PA (HARD) HARVARD COLLEGE.
 PA (STRD) UNIV LELAND S STANFORD.
 XX
 PI Chang H;
 XX
 DR WPI; 1997-192900/17.
 DR P-PSDB; AAW27537.
 XX
 PT Rat and human cerebellum-derived growth factors - used in the treatment
 PT of neuronal injury and proliferative disorders.
 XX
 PS Claim 17; Page 70-74; 94pp; English.
 XX
 CC The present sequence encodes rat cerebellum derived growth factor 2
 CC (CDGF2), which can be used to screen for modulators of CDGF binding to
 CC erbB type receptors. Identification of a modification or mutation in a
 CC CDGF gene, or aberrant expression of a CDGF gene or levels of soluble
 CC CDGF may be used to indicate the risk of unwanted cell proliferation or
 CC differentiation. CDGF may be used to induce neuronal differentiation in
 CC stem cell culture, and maintain the integrity of a terminally
 CC differentiated neuronal cell culture, e.g. useful for intracerebral
 CC grafting to alleviate behavioural defects. CDGF may also be used in nerve
 CC prostheses to repair central and peripheral nerve damage, especially where
 CC a crushed or severed axon is entubulated by a prosthetic. CDGF may also
 CC be used to enhance neuronal cell survival in the central or peripheral
 CC nervous system, to treat neurological conditions associated with nervous
 CC system injury, e.g. traumatic, chemical or vasal injury and deficits such
 CC as ischaemia resulting from stroke, infectious/inflammatory and tumour
 CC induced injury, chronic neurodegenerative disease including Parkinson's
 CC and Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar
 CC degeneration, chronic immunological disease of the nervous system
 CC including multiple sclerosis, disorders of the sensory neurons and
 CC degenerative diseases of the retina. CDGF may also be used to treat
 CC neoplastic or hyperplastic transformations, particularly of the central
 CC nervous system, e.g. amalignant gliomas, medulloblastomas and
 CC neuroectodermal tumours
 XX
 SQ Sequence 1803 BP; 408 A; 549 C; 537 G; 309 T; 0 U; 0 Other;

Query Match 88.7%; Score 882; DB 2; Length 1803;
 Best Local Similarity 93.0%; Pred. No. 6.2e-203;

Matches 924; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
      |||
Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 60

Qy     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db     61 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
Db    121 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 180

Qy    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
      |||
Db    181 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

Qy    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG 300
      |||
Db    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCG 300

Qy    301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
      |||
Db    301 CGCTACATCTTTTTCTGGAGCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 360

Qy    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
      |||
Db    361 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

Qy    421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
      |||
Db    421 TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 480

Qy    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
      |||
Db    481 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCAGCCCTCCTATCGATGGTTCAAG 540

Qy    541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
      |||
Db    541 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG 600

Qy    601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
      |||
Db    601 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 660

Qy    661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
      |||
Db    661 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCGGCTCCATGTCAACAGTGTGAGC 720

Qy    721 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
      |||
Db    721 ACCACTCTGTCGTCCTGGTCGGGGCAGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 780

Qy    781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
      |||
Db    781 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 840
```

QY 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCA 900
 ||||| ||||||||||||||||||||||||||||||||||||||||||||
 Db 841 CCAAACGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCA 900
 QY 901 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 960
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 901 GATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGG 960
 QY 961 TCAACTTCTCCAAGCACCTTGGATTGGAATTAAA 994
 ||||||||||||||||||||||||||||
 Db 961 TCAACTTCTCCAAGCACCTTGGATTGGAATTAAA 994

RESULT 4

AAS18020

ID AAS18020 standard; cDNA; 897 BP.

XX

AC AAS18020;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human cDNA encoding Neuregulin-2beta, NRG-2beta.

XX

KW Human; ss; neuregulin-2; NRG-2alpha; NRG-2beta; mitogenesis;
 KW cell survival; cell growth; cell differentiation; erbB receptor;
 KW cardiomyopathy; ischaemic damage; cardiac trauma; heart failure;
 KW atherosclerosis; vascular lesion; vascular hypertension;
 KW degenerative congenital vascular disease; myasthenia gravis;
 KW neurodegenerative disorder; peripheral neuropathy;
 KW sensory nerve fiber neuropathy; motor fiber neuropathy;
 KW sensory nerve fiber neuropathy; multiple sclerosis;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve injury;
 KW Alzheimer's disease; Parkinson's disease; cerebellar ataxia;
 KW spinal cord injury; tumour; neurofibromatosis; transgenic animal.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT CDS 1. .897
 FT /*tag= a
 FT /product= "NRG-2beta"

XX

PN WO200189568-A1.

XX

PD 29-NOV-2001.

XX

PF 23-MAY-2001; 2001WO-US016896.

XX

PR 23-MAY-2000; 2000US-0206495P.

XX

PA (CENE-) CENES PHARM INC.

XX

PI Marchionni MA;

XX

DR WPI; 2002-097612/13.

DR P-PSDB; AAU11636.

XX
PT Neuregulin-2 polypeptide and polynucleotide useful for treating multiple
PT sclerosis, spinal muscular atrophy, nerve injury, Alzheimer's disease, by
PT increasing mitogenesis, survival, growth or differentiation of a cell.
XX
PS Claim 57; Fig 8; 79pp; English.
XX
CC The invention relates to a substantially pure neuregulin (NRG)-2
CC polypeptide comprising or consisting of a sequence for human NRG-2alpha
CC or NRG-2beta (clone 2b7) and the polynucleotides encoding the. Also
CC included are a vector expressing the protein, a host cell comprising the
CC vector, a transgenic non-human animal transformed with the vector or
CC having a knockout mutation in one or both NRG-2 alleles and an anti-NRG-2
CC antibody. Analysis of mutations in NRG-2 in an individual is useful for
CC diagnosing an increased likelihood of developing a NRG-2-related disease
CC or condition in a test subject. NRG-2 is useful for increasing the
CC mitogenesis, survival, growth or differentiation of a cell (e.g. a
CC neuronal cell), where the cell expresses an erbB receptor. NRG-2 is
CC useful for treating diseases and disorders such as cardiomyopathy
CC (preferably degenerative congenital disease), ischaemic damage, cardiac
CC trauma or heart failure or which has a condition affecting smooth muscle
CC which include atherosclerosis, vascular lesion, vascular hypertension,
CC and degenerative congenital vascular disease, myasthenia gravis, a
CC neurodegenerative disorder, peripheral neuropathy, a sensory nerve fiber
CC neuropathy, a motor fiber and a sensory nerve fiber neuropathy, multiple
CC sclerosis, amyotrophic lateral sclerosis, spinal muscular atrophy, nerve
CC injury, Alzheimer's disease, Parkinson's disease, cerebellar ataxia, and
CC spinal cord injury. The antibody is useful for treatment of a tumour
CC comprising inhibiting proliferation of a tumour cell preferably a glial
CC tumour cell, for treating of neurofibromatosis by inhibiting glial cell
CC mitogenesis. The present sequence encodes NRG-2beta
XX
SQ Sequence 897 BP; 200 A; 261 C; 282 G; 154 T; 0 U; 0 Other;

Query Match 85.4%; Score 849; DB 6; Length 897;
Best Local Similarity 98.3%; Pred. No. 4.7e-195;
Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300

Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTTCAAG	540
Db	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600
Db	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTGCGATCAAATATGGCAACGGCAGAAAG	600
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
Db	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
Qy	841	CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	873
Db	841	CCTGTGGGATACACCGGGGACAGGTGTCAGCAG	873

RESULT 5

AAV43674

ID AAV43674 standard; cDNA; 3076 BP.

XX

AC AAV43674;

XX

DT 29-SEP-1998 (first entry)

XX

DE Receptor type tyrosine kinase ErbB ligand encoding cDNA.

XX

KW Receptor type tyrosine kinase ErbB; ligand; diagnostic agent;
 KW nervous disease; cancer; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers
 FT CDS 232..2814
 FT /*tag= a
 FT /product= "ligand of receptor type tyrosine kinase ErbB"
 XX
 PN JP10179166-A.
 XX
 PD 07-JUL-1998.
 XX
 PF 25-DEC-1996; 96JP-00356998.
 XX
 PR 25-DEC-1996; 96JP-00356998.
 XX
 PA (HIGA/) HIGASHIYAMA S.
 XX
 DR WPI; 1998-430952/37.
 DR P-PSDB; AAW63700.
 XX
 PT Gene coding the ligand of the tyrosine kinase ErbB receptor - useful for
 PT diagnosing and treating nervous diseases and cancer.
 XX
 PS Example; Page 9-13; 17pp; Japanese.
 XX
 CC This cDNA encodes the ligand of receptor type tyrosine kinase ErbB. A
 CC prokaryotic or eukaryotic host cell transformed by a recombinant vector
 CC containing the encoding DNA can be used for the recombinant production of
 CC the protein. The invention provides a method for inhibiting the formation
 CC of the ligand of receptor type tyrosine kinase ErbB in an animal using an
 CC antibody recognizing the protein. The ligand of the tyrosine kinase ErbB
 CC receptor and associated materials can be used for treating or diagnosing
 CC nervous diseases and cancers
 XX
 SQ Sequence 3076 BP; 673 A; 996 C; 944 G; 463 T; 0 U; 0 Other;

Query Match 80.4%; Score 799.4; DB 2; Length 3076;
 Best Local Similarity 92.2%; Pred. No. 6.3e-183;
 Matches 842; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
 ||||||||||||||||||||||||| ||| ||||||||||||||||||| |||||||||
 Db 556 ATGAGGCGCGACCCGGCCCCCGGCTCCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 615
 QY 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 ||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||
 Db 616 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 675
 QY 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||||||||||||||| |||| ||| ||| ||||| ||||||||| |||||||||
 Db 676 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTCCAGCTCTAACAGCACCCGAGAGCCT 735
 QY 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||||||||||||||||||| |||| ||||||||||||||||||||||||| |||||||||
 Db 736 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 795
 QY 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 ||||||||||||||||||||||||||||||||||||| |||||||||||||||||
 Db 796 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 855

Qy 301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 856 CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC 915
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 || |||
 Db 916 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 975
 Qy 421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 |||
 Db 976 TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 1035
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 || |||
 Db 1036 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCCTATCGATGGTTCAAG 1095
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
 || |||
 Db 1096 GACGGCAAGGAGCTCAACCGGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG 1155
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||
 Db 1156 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 1215
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 || |||
 Db 1216 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 1275
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCTTAT 780
 |||
 Db 1276 ACCACTCTGTCTCCTGGTCGGGGCAGCCCCGGAAGTGCAATGAGACAGCCAAGTCTTAC 1335
 Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 || |||
 Db 1336 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGT 1395
 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
 |||
 Db 1396 CCAAACGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1455
 Qy 901 GATCCTAAGCAAA 913
 |||
 Db 1456 GATCCTAAGCAAA 1468

RESULT 6

ABS56035

ID ABS56035 standard; cDNA; 1863 BP.

XX

AC ABS56035;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding human membrane-bound splice variant of Don-1.

XX

KW Human; Don-1; epidermal growth factor; EGF; neuregulin;

KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 643..1863
 FT /*tag= a
 FT /partial
 FT /product= "Membrane-bound splice variant of Don-1"
 FT /note= "This sequence lacks a stop codon"
 XX
 PN US2002127594-A1.
 XX
 PD 12-SEP-2002.
 XX
 PF 12-MAR-2002; 2002US-00096241.
 XX
 PR 22-JUN-2000; 2000US-00599789.
 XX
 PA (GEAR/) GEARING D P.
 PA (BUSF/) BUSFIELD S J.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 2003-039584/03.
 DR P-PSDB; ABG71638.
 XX
 PT Novel Don-1 polypeptide useful for stimulating proliferation of cells,
 PT for identifying proteins that interact with Don-1, and for regulating
 PT tumor formation and progression in brain.
 XX
 PS Claim 4; Fig 3; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel gene called Don
 CC -1, and alternate splice variants of Don-1, which are related to
 CC epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides
 CC are glycoprotein ligands. Both murine and human Don-1 sequences are
 CC cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides
 CC are useful for stimulating proliferation of a cell. Antibodies to Don-1
 CC polypeptides are useful for detecting Don-1 in a sample. The Don-1
 CC polypeptides are useful for treating and diagnosing cell proliferative
 CC disorders and play a role in the proliferation of carcinomas e.g.
 CC adenocarcinoma, myeloma, in cell differentiation, proliferation and
 CC survival. The polypeptides are also useful for inhibiting proliferation
 CC of adenocarcinoma cells, for stimulating the proliferation of cells such
 CC as epithelial cells to promote wound healing, for identifying proteins
 CC that interact with Don-1, and for regulating tumour formation and
 CC progression in the brain. The polynucleotide sequences encoding Don-1 may
 CC be used in gene therapy. The present sequence encodes human membrane-
 CC bound splice variant of Don-1
 XX
 SQ Sequence 1863 BP; 422 A; 602 C; 553 G; 286 T; 0 U; 0 Other;

Query Match

79.3%; Score 788; DB 7; Length 1863;

Best Local Similarity 97.6%; Pred. No. 3.1e-180;
Matches 898; Conservative 0; Mismatches 5; Indels 17; Gaps 9;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
      |||
Db     213 ATGAGGCGCGACCCGGCCCCC--CTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 270

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
      |||
Db     271 TACTCGCCAGCCTCAAGTCA--GCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 328

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
      |||
Db     329 GGCAAGGTACAGGGGCTGGT--CAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 386

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
      |||
Db     387 CCCGCCTCGGGTCGGGTGGCG--GGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 444

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG 300
      |||
Db     445 GGGCTGCAGCGCGAGCAGGTG--CAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCG 502

Qy     301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
      |||
Db     503 CGCTACATCTTTTTCCTGGAG--CACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 560

Qy     361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
      |||
Db     561 CCCCT-GATACCAACGGCAAAA--CTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 617

Qy     421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
      |||
Db     618 TGCGCCACCCGGCCCCAAGTTGA--AAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 675

Qy     481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
      |||
Db     676 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 735

Qy     541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 600
      |||
Db     736 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 795

Qy     601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
      |||
Db     796 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 855

Qy     661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
      |||
Db     856 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 915

Qy     721 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCTTAT 780
      |||
Db     916 ACCACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCTTAT 975

Qy     781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
      |||
```

Db 976 TGGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1035

QY 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCA 900
 |||

Db 1036 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCA 1095

QY 901 GATCCTAAGCAAAGTGTCT 920
 |||

Db 1096 GATCCTAAGCAAAAGCACCT 1115

RESULT 7

AAT87922

ID AAT87922 standard; cDNA; 3441 BP.

XX

AC AAT87922;

XX

DT 18-DEC-1997 (first entry)

XX

DE Rat cerebellum derived growth factor 1 cDNA.

XX

KW Rat; cerebellum derived growth factor; CDGF1; screening; binding;
 KW modulation; erbB type receptor; identification; indication; risk;
 KW proliferation; differentiation; induction; neuron; hyperplasia;
 KW stem cell culture; intracerebral graft; alleviation; repair;
 KW behavioural defect; nervous system; central; peripheral; nerve;
 KW prothesis; damage; entubulation; cell survival; treatment; injury;
 KW trauma; ischaemia; ischemia; stroke; infection; disorder; inflammation;
 KW neurodegeneration; disease; Parkinson's; Huntingdon's;
 KW amyotrophic lateral sclerosis; sensory; retina;
 KW spinocerebellar degeneration; multiple sclerosis; neoplasia;
 KW amalignant glioma; medulloblastoma; neuroectodermal tumour; ds.

XX

OS Rattus rattus.

XX

FH Key Location/Qualifiers

FT CDS 180. .2444

FT /*tag= a

FT sig_peptide 180. .248

FT /*tag= b

FT mat_peptide 249. .2441

FT /*tag= c

FT /product= "cerebellum_derived_growth_factor"

XX

PN WO9709425-A1.

XX

PD 13-MAR-1997.

XX

PF 09-SEP-1996; 96WO-US014484.

XX

PR 08-SEP-1995; 95US-00525864.

XX

PA (HARD) HARVARD COLLEGE.

PA (STRD) UNIV LELAND S STANFORD.

XX

PI Chang H;

XX

DR WPI; 1997-192900/17.

DR P-PSDB; AAW27536.

XX

PT Rat and human cerebellum-derived growth factors - used in the treatment
PT of neuronal injury and proliferative disorders.

XX

PS Claim 17; Page 63-66; 94pp; English.

XX

CC The present sequence encodes rat cerebellum derived growth factor 1
CC (CDGF1), which can be used to screen for modulators of CDGF binding to
CC erbB type receptors. Identification of a modification or mutation in a
CC CDGF gene, or aberrant expression of a CDGF gene or levels of soluble
CC CDGF may be used to indicate the risk of unwanted cell proliferation or
CC differentiation. CDGF may be used to induce neuronal differentiation in
CC stem cell culture, and maintain the integrity of a terminally
CC differentiated neuronal cell culture, e.g. useful for intracerebral
CC grafting to alleviate behavioural defects. CDGF may also be used in nerve
CC protheses to repair central and peripheral nerve damage, especially where
CC a crushed or severed axon is entubulated by a prosthetic. CDGF may also
CC be used to enhance neuronal cell survival in the central or peripheral
CC nervous system, to treat neurological conditions associated with nervous
CC system injury, e.g. traumatic, chemical or vasal injury and deficits such
CC as ischaemia resulting from stroke, infectious/inflammatory and tumour
CC induced injury, chronic neurodegenerative disease including Parkinson's
CC and Huntingdon's, amyotrophic lateral sclerosis, spinocerebellar
CC degeneration, chronic immunological disease of the nervous system
CC including multiple sclerosis, disorders of the sensory neurons and
CC degenerative diseases of the retina. CDGF may also be used to treat
CC neoplastic or hyperplastic transformations, particularly of the central
CC nervous system, e.g. amalignant gliomas, medulloblastomas and
CC neuroectodermal tumours

XX

SQ Sequence 3441 BP; 777 A; 1057 C; 1015 G; 592 T; 0 U; 0 Other;

Query Match 74.3%; Score 738.6; DB 2; Length 3441;

Best Local Similarity 90.4%; Pred. No. 3.1e-168;

Matches 789; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

```
Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCTCGCTCGCCTGC 60
          |||
Db      180 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239

Qy      61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
          |||
Db      240 TACTCGCCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299

Qy     121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
          |||
Db     300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 359

Qy     181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
          |||
Db     360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419

Qy     241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
          |||
Db     420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
```

Qy	301	CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	480	CGCTACATCTTTTTCCTGGAGCCCACCGAGCAGCCCTTAGTTTTTAAGACAGCCTTTGCC	539
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	540	CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	599
Qy	421	TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	600	TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG	659
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCTACCGTTGGTTCAAG	540
Db	660	CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCCAGCCCTCTATCGATGGTTCAAG	719
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	720	GACGGCAAGGAGCTCAACCGGAGTCGTGACATTTCGCATCAAGTATGGCAACGGCAGAAAG	779
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	780	AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG	839
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	840	GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC	899
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCAGTGAACGAGACAGCCAAGTCCTAT	780
Db	900	ACCACTCTGTCTGCTGCTGGTCGGGGCACGCCCAGTGAATGAGACAGCCAAGTCCTAC	959
Qy	781	TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCTGCAAATGT	840
Db	960	TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCTGCAAGTGT	1019
Qy	841	CCAAATGGATTCTTCGGACAGAGATGTTTGGAG	873
Db	1020	CCTGTGGGATACACGGGGACAGGTGTCAGCAG	1052

RESULT 8

AAV17813

ID AAV17813 standard; cDNA; 1607 BP.

XX

AC AAV17813;

XX

DT 17-AUG-1998 (first entry)

XX

DE Mus musculus don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;
 KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
 KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
 KW wound healing; secreted protein; ss.

XX

```
OS      Mus musculus.
XX
FH      Key                Location/Qualifiers
FT      CDS                79..624
FT                      /*tag=   a
FT                      /note= "secreted don-1 polypeptide"
XX
PN      WO9807736-A1.
XX
PD      26-FEB-1998.
XX
PF      18-AUG-1997;       97WO-US014585.
XX
PR      19-AUG-1996;       96US-00699591.
PR      19-NOV-1996;       96US-00753007.
XX
PA      (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI      Gearing DP, Busfield SJ;
XX
DR      WPI; 1998-169084/15.
DR      P-PSDB; AAW48380.
XX
PT      Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
PT      and adenocarcinoma(s), and for wound healing.
XX
PS      Claim 4; Fig 2; 121pp; English.
XX
CC      The sequence is that of a murine don-1 gene splice variant. Don-1
CC      polypeptides stimulate proliferation of epithelial cells and thus are
CC      implicated in melanomas and adenocarcinomas in which epithelial cells
CC      proliferate out of control. Compounds that interfere with don-1 mediated
CC      cell proliferation can be used in the treatment of tumours such as
CC      melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
CC      liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
CC      Alternatively, don-1 polypeptides can be used to stimulate epithelial
CC      cell proliferation, e.g. for wound healing
XX
SQ      Sequence 1607 BP; 365 A; 500 C; 480 G; 262 T; 0 U; 0 Other;

Query Match          55.1%; Score 547.2; DB 2; Length 1607;
Best Local Similarity 92.3%; Pred. No. 4e-122;
Matches 576; Conservative    0; Mismatches 48; Indels    0; Gaps    0;

QY      371 CCAACGGCAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2   CTAACGGCAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

QY      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      62  GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

QY      491 AGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
        ||||| ||||| || || || ||||| ||||| || ||||| ||||| ||||| |||||
Db     122 AGTGTGAGGCAGCGCGGAAACCCCAGCCCTCCTATCGCTGTTCAAGGATGGCAAGG 181

QY      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
```

Db	182	AACTCAACCGGAGTCGTGATATTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC	241
Qy	611	TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA	670
Db	242	TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA	301
Qy	671	TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT	730
Db	302	TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCCTCTGT	361
Qy	731	CATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTATTGCGTCAATG	790
Db	362	CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCTACTGTGTGAATG	421
Qy	791	GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGAT	850
Db	422	GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT	481
Qy	851	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC	910
Db	482	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC	541
Qy	911	AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC	970
Db	542	AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC	601
Qy	971	CAAGCACCTTGGATTTGAATTAAA	994
Db	602	CAAGCACCTTGGATTTGAATTGAA	625

RESULT 9

ABS56034

ID ABS56034 standard; cDNA; 1561 BP.

XX

AC ABS56034;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding murine secreted splice variant of Don-1.

XX

KW Murine; Don-1; epidermal growth factor; EGF; neuregulin; mouse;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; chromosome 18; gene; ss.

XX

OS Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 78..623

FT /*tag= a

FT /product= "Secreted splice variant of Don-1"

XX

PN US2002127594-A1.

XX

XX
 PF 18-AUG-1997; 97WO-US014585.
 XX
 PR 19-AUG-1996; 96US-00699591.
 PR 19-NOV-1996; 96US-00753007.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 1998-169084/15.
 DR P-PSDB; AAW48383.
 XX
 PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.
 XX
 PS Claim 4; Fig 7; 121pp; English.
 XX
 CC The sequence is that of a human don-1 gene splice variant. Don-1
 CC polypeptides stimulate proliferation of epithelial cells and thus are
 CC implicated in melanomas and adenocarcinomas in which epithelial cells
 CC proliferate out of control. Compounds that interfere with don-1 mediated
 CC cell proliferation can be used in the treatment of tumours such as
 CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
 CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
 CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
 CC cell proliferation, e.g. for wound healing
 XX
 SQ Sequence 2268 BP; 502 A; 735 C; 700 G; 331 T; 0 U; 0 Other;

Query Match 49.5%; Score 492; DB 2; Length 2268;
 Best Local Similarity 92.8%; Pred. No. 9.4e-109;
 Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy	363	CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG	422
Db	98	CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA	157
Qy	423	CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	482
Db	158	AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA	217
Qy	483	ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	542
Db	218	ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA	277
Qy	543	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	602
Db	278	TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA	337
Qy	603	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	662
Db	338	CTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC	397
Qy	663	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	722
Db	398	CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC	457

QY 723 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
 |||
 Db 458 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
 QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
 |||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 QY 843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 902
 |||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 637
 QY 903 TCCTAAGCAAAGTGTC 918
 |||
 Db 638 TCCTAAGCAAAAAGCC 653

RESULT 11

ABS56036

ID ABS56036 standard; cDNA; 1474 BP.

XX

AC ABS56036;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding human second splice variant of Don-1.

XX

KW Human; Don-1; epidermal growth factor; EGF; neuregulin;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 68. .1473

FT /*tag= a

FT /partial

FT /product= "Second splice variant of Don-1"

FT /note= "This sequence lacks a stop codon"

FT /transl_except= (pos:107. .108, aa:Lys)

FT /note= "This codon has an apparent 1 nucleotide deletion
 which alters the reading frame"

XX

PN US2002127594-A1.

XX

PD 12-SEP-2002.

XX

PF 12-MAR-2002; 2002US-00096241.

XX

PR 22-JUN-2000; 2000US-00599789.

XX

PA (GEAR/) GEARING D P.

PA (BUSF/) BUSFIELD S J.

XX


```

Db      421 GTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGTCATCCTGGTCGGGGGCAC 480
QY      748 GCCCAGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 807
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GCCCAGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 540
QY      808 ATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGT 867
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 ATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGT 600
QY      868 TTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAAGTGTC 918
        |||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAAAAGCC 651

```

RESULT 12

ABS56045

ID ABS56045 standard; cDNA; 2266 BP.

XX

AC ABS56045;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding human third splice variant of Don-1.

XX

KW Human; Don-1; epidermal growth factor; EGF; neuregulin;
KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
KW cell survival; epithelial cell; wound healing; tumour formation; brain;
KW vulnerary; cytostatic; gene therapy; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 68. .2010

FT /*tag= a

FT /product= "Third splice variant of Don-1"

FT /transl_except= (pos:107. .108, aa:Lys)

FT /note= "This codon has an apparent 1 nucleotide deletion
which alters the reading frame"

FT /transl_except= (pos:994. .996, aa:Thr)

XX

PN US2002127594-A1.

XX

PD 12-SEP-2002.

XX

PF 12-MAR-2002; 2002US-00096241.

XX

PR 22-JUN-2000; 2000US-00599789.

XX

PA (GEAR/) GEARING D P.

PA (BUSF/) BUSFIELD S J.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 2003-039584/03.

DR P-PSDB; ABG71644.

Db 481 GCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATGGAGGCGTCTGCTACTAC 540

Qy 808 ATCGAGGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGT 867
 |||

Db 541 ATCGAGGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGT 600

Qy 868 TTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAAGTGTC 918
 |||

Db 601 TTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCAAAAAGCC 651

RESULT 13

AAV17815

ID AAV17815 standard; cDNA; 1476 BP.

XX

AC AAV17815;

XX

DT 17-AUG-1998 (first entry)

XX

DE Homo sapiens don-1 gene splice variant.

XX

KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;
 KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
 KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
 KW wound healing; transmembrane; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 69. .1475

FT /*tag= a

FT /note= "don-1 polypeptide"

XX

PN WO9807736-A1.

XX

PD 26-FEB-1998.

XX

PF 18-AUG-1997; 97WO-US014585.

XX

PR 19-AUG-1996; 96US-00699591.

PR 19-NOV-1996; 96US-00753007.

XX

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX

PI Gearing DP, Busfield SJ;

XX

DR WPI; 1998-169084/15.

DR P-PSDB; AAW48382.

XX

PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.

XX

PS Claim 4; Fig 4; 121pp; English.

XX

CC The sequence is that of a human don-1 gene splice variant. Don-1
 CC polypeptides stimulate proliferation of epithelial cells and thus are
 CC implicated in melanomas and adenocarcinomas in which epithelial cells

CC proliferate out of control. Compounds that interfere with don-1 mediated
 CC cell proliferation can be used in the treatment of tumours such as
 CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
 CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
 CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
 CC cell proliferation, e.g. for wound healing

XX

SQ Sequence 1476 BP; 335 A; 475 C; 450 G; 216 T; 0 U; 0 Other;

Query Match 49.3%; Score 490.4; DB 2; Length 1476;
 Best Local Similarity 92.6%; Pred. No. 2e-108;
 Matches 515; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
          || || | || | | | | | | | | | | | | | | | | | | | | | | |
Db      98  CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      458 CACCCTGTTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy      843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 902
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      578 AAATGGATTCTTCGCACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 637

Qy      903 TCCTAAGCAAAGTGTC 918
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      638 TCCTAAGCAAAAAGCC 653
  
```

RESULT 14

AAV17812

ID AAV17812 standard; cDNA; 2467 BP.

XX
 AC AAV17812;
 XX
 DT 17-AUG-1998 (first entry)
 XX
 DE Mus musculus don-1 gene splice variant.
 XX
 KW Murine; don-1 gene; melanoma; treatment; adenocarcinoma; epithelial cell;
 KW proliferation; stimulation; treatment; tumours; skin; oesophagus; lung;
 KW breast; liver; pancreas; colon; prostate; gastrointestinal tract; uterus;
 KW wound healing; transmembrane; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 79..1896
 FT /*tag= a
 FT /note= "transmembrane don-1 polypeptide"
 XX
 PN WO9807736-A1.
 XX
 PD 26-FEB-1998.
 XX
 PF 18-AUG-1997; 97WO-US014585.
 XX
 PR 19-AUG-1996; 96US-00699591.
 PR 19-NOV-1996; 96US-00753007.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Gearing DP, Busfield SJ;
 XX
 DR WPI; 1998-169084/15.
 DR P-PSDB; AAW48379.
 XX
 PT Mouse and human don-1 polypeptide(s) - useful for treatment of melanomas
 PT and adenocarcinoma(s), and for wound healing.
 XX
 PS Claim 4; Fig 1; 121pp; English.
 XX
 CC The sequence is that of a murine don-1 gene splice variant. Don-1
 CC polypeptides stimulate proliferation of epithelial cells and thus are
 CC implicated in melanomas and adenocarcinomas in which epithelial cells
 CC proliferate out of control. Compounds that interfere with don-1 mediated
 CC cell proliferation can be used in the treatment of tumours such as
 CC melanomas and adenocarcinomas of the skin, oesophagus, lung, breast,
 CC liver, pancreas, gastrointestinal tract, colon, prostate or uterus.
 CC Alternatively, don-1 polypeptides can be used to stimulate epithelial
 CC cell proliferation, e.g. for wound healing
 XX
 SQ Sequence 2467 BP; 592 A; 752 C; 706 G; 417 T; 0 U; 0 Other;

Query Match 46.7%; Score 464.6; DB 2; Length 2467;
 Best Local Similarity 91.0%; Pred. No. 4e-102;
 Matches 494; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430

Db	2	CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC	61
Qy	431	GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA	490
Db	62	GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA	121
Qy	491	AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG	550
Db	122	AGTGTGAGGCAGCGGCGGGAACCCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG	181
Qy	551	AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC	610
Db	182	AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTCAGAAAGAACTCACGGC	241
Qy	611	TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA	670
Db	242	TACAGTTCAACAAAGTGAGCGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA	301
Qy	671	TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT	730
Db	302	TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGACCACCACTCTGT	361
Qy	731	CATCCTGGTCGGGGCACGCCCCGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG	790
Db	362	CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG	421
Qy	791	GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGAT	850
Db	422	GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT	481
Qy	851	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC	910
Db	482	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC	541
Qy	911	AAA	913
Db	542	AAA	544

RESULT 15

ABS56033

ID ABS56033 standard; cDNA; 2442 BP.

XX

AC ABS56033;

XX

DT 14-JAN-2003 (first entry)

XX

DE cDNA encoding murine membrane-bound splice variant of Don-1.

XX

KW Murine; Don-1; epidermal growth factor; EGF; neuregulin; mouse;
 KW glycoprotein ligand; cell proliferation; cell proliferative disorder;
 KW carcinoma; adenocarcinoma cell; myeloma; cell differentiation;
 KW cell survival; epithelial cell; wound healing; tumour formation; brain;
 KW vulnerary; cytostatic; gene therapy; chromosome 18; gene; ss.

XX

OS Mus sp.

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XX
FH   Key                Location/Qualifiers
FT   CDS                78..1895
FT                                  /*tag= a
FT                                  /product= "Membrane-bound splice variant of Don-1"
XX
PN   US2002127594-A1.
XX
PD   12-SEP-2002.
XX
PF   12-MAR-2002; 2002US-00096241.
XX
PR   22-JUN-2000; 2000US-00599789.
XX
PA   (GEAR/) GEARING D P.
PA   (BUSF/) BUSFIELD S J.
XX
PI   Gearing DP, Busfield SJ;
XX
DR   WPI; 2003-039584/03.
DR   P-PSDB; ABG71636.
XX
PT   Novel Don-1 polypeptide useful for stimulating proliferation of cells,
PT   for identifying proteins that interact with Don-1, and for regulating
PT   tumor formation and progression in brain.
XX
PS   Claim 4; Fig 1; 66pp; English.
XX
CC   The present invention relates to the isolation of a novel gene called Don
CC   -1, and alternate splice variants of Don-1, which are related to
CC   epidermal growth factors (EGF) such as neuregulins. Don-1 polypeptides
CC   are glycoprotein ligands. Both murine and human Don-1 sequences are
CC   cloned. The mouse Don-1 gene maps to chromosome 18. Don-1 polypeptides
CC   are useful for stimulating proliferation of a cell. Antibodies to Don-1
CC   polypeptides are useful for detecting Don-1 in a sample. The Don-1
CC   polypeptides are useful for treating and diagnosing cell proliferative
CC   disorders and play a role in the proliferation of carcinomas e.g.
CC   adenocarcinoma, myeloma, in cell differentiation, proliferation and
CC   survival. The polypeptides are also useful for inhibiting proliferation
CC   of adenocarcinoma cells, for stimulating the proliferation of cells such
CC   as epithelial cells to promote wound healing, for identifying proteins
CC   that interact with Don-1, and for regulating tumour formation and
CC   progression in the brain. The polynucleotide sequences encoding Don-1 may
CC   be used in gene therapy. The present sequence encodes murine membrane-
CC   bound splice variant of Don-1
XX
SQ   Sequence 2442 BP; 587 A; 742 C; 703 G; 410 T; 0 U; 0 Other;

Query Match                45.9%; Score 455.8; DB 7; Length 2442;
Best Local Similarity      91.2%; Pred. No. 5.3e-100;
Matches 495; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

Qy      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
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Db      2   CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCA-CC 60

Qy      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490

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OM nucleic - nucleic search, using sw model

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(without alignments)
6065.966 Million cell updates/sec

Title: US-09-864-675-1
Perfect score: 994
Sequence: 1 atgaggcgcgacccggcccc.....caccttggaattgaattaaa 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	900	90.5	1884	3	US-08-753-007A-5	Sequence 5, Appli
2	900	90.5	1884	3	US-09-398-496-5	Sequence 5, Appli
3	881	88.6	993	2	US-08-525-864A-3	Sequence 3, Appli
4	738.6	74.3	3441	2	US-08-525-864A-1	Sequence 1, Appli
5	547.2	55.1	1607	3	US-08-753-007A-3	Sequence 3, Appli
6	547.2	55.1	1607	3	US-09-398-496-3	Sequence 3, Appli
7	492	49.5	1476	3	US-08-753-007A-7	Sequence 7, Appli
8	492	49.5	1476	3	US-09-398-496-7	Sequence 7, Appli
9	492	49.5	2268	3	US-08-753-007A-31	Sequence 31, Appl
10	492	49.5	2268	3	US-09-398-496-31	Sequence 31, Appl
11	467.8	47.1	2467	3	US-08-753-007A-1	Sequence 1, Appli

12	467.8	47.1	2467	3	US-09-398-496-1	Sequence 1, Appli
13	359.6	36.2	1207	2	US-08-525-864A-5	Sequence 5, Appli
14	135.6	13.6	142	2	US-08-525-864A-18	Sequence 18, Appl
15	95.4	9.6	1140	1	US-08-036-555B-149	Sequence 149, App
16	95.4	9.6	1140	1	US-08-469-569-149	Sequence 149, App
17	95.4	9.6	1140	1	US-08-249-322A-149	Sequence 149, App
18	95.4	9.6	1140	1	US-08-469-526A-149	Sequence 149, App
19	95.4	9.6	1140	2	US-08-734-591A-149	Sequence 149, App
20	95.4	9.6	1140	2	US-08-469-660-149	Sequence 149, App
21	95.4	9.6	1140	3	US-08-341-018-55	Sequence 55, Appl
22	95.4	9.6	1140	3	US-08-470-335-149	Sequence 149, App
23	95.4	9.6	1140	3	US-08-735-021-149	Sequence 149, App
24	95.4	9.6	1140	3	US-08-734-664A-149	Sequence 149, App
25	95.4	9.6	1140	3	US-08-470-339-149	Sequence 149, App
26	95.4	9.6	1140	4	US-08-467-602-149	Sequence 149, App
27	95.4	9.6	1140	5	PCT-US94-05083C-145	Sequence 145, App
28	95.4	9.6	1140	5	PCT-US95-06846A-149	Sequence 149, App
29	93.4	9.4	1193	1	US-08-469-526A-134	Sequence 134, App
30	93.4	9.4	1193	2	US-08-734-591A-134	Sequence 134, App
31	93.4	9.4	1193	3	US-08-341-018-3	Sequence 3, Appli
32	93.4	9.4	1193	3	US-08-470-335-134	Sequence 134, App
33	93.4	9.4	1193	3	US-08-735-021-134	Sequence 134, App
34	93.4	9.4	1193	3	US-08-734-664A-134	Sequence 134, App
35	93.4	9.4	1193	3	US-08-470-339-134	Sequence 134, App
36	93.4	9.4	1193	4	US-08-467-602-134	Sequence 134, App
37	91.8	9.2	1193	1	US-08-036-555B-134	Sequence 134, App
38	91.8	9.2	1193	1	US-08-469-569-134	Sequence 134, App
39	91.8	9.2	1193	1	US-08-249-322A-134	Sequence 134, App
40	91.8	9.2	1193	2	US-08-469-660-134	Sequence 134, App
41	91.8	9.2	1193	5	PCT-US94-05083C-130	Sequence 130, App
42	91.8	9.2	1193	5	PCT-US95-06846A-134	Sequence 134, App
43	78.2	7.9	1027	4	US-09-684-708A-26	Sequence 26, Appl
44	78.2	7.9	3086	4	US-09-684-708A-20	Sequence 20, Appl
45	77.4	7.8	2003	1	US-08-036-555B-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-08-753-007A-5

; Sequence 5, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/753,007A
; FILING DATE: 19-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1884 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 664...1883
; OTHER INFORMATION:
US-08-753-007A-5

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Query Match          90.5%; Score 900; DB 3; Length 1884;
Best Local Similarity 99.3%; Pred. No. 4.7e-225;
Matches 914; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      218 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db      278 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 337

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db      338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db      398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517

Qy      301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

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Db      518  |||||CGCTACATCTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
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Db      578  |||||CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636
Qy      421  TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Qy      481  CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
Db      697  |||||CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
Qy      541  GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
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Db      817  |||||AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
Qy      661  GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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Qy      721  ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
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Qy      781  TCGCTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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RESULT 2

US-09-398-496-5

; Sequence 5, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

Db 398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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 Db 458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517
 Qy 301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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 Db 518 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Db 578 CCCCT-GATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGGC 636
 Qy 421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAAG 816
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 Db 817 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 876
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
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 Db 937 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
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 Db 1117 GATCCTAAGCAAAGCACCT 1136

RESULT 3

US-08-525-864A-3

; Sequence 3, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

```

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses
; TITLE OF INVENTION: Related thereto
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,864A
; FILING DATE: 8-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..990
US-08-525-864A-3

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Query Match          88.6%; Score 881; DB 2; Length 993;
Best Local Similarity 93.0%; Pred. No. 3.3e-220;
Matches 923; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Qy    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db    121 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 180

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; Patent No. 5912326
; GENERAL INFORMATION:
; APPLICANT: Chang, Han
; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses
; TITLE OF INVENTION: Related thereto
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,864A
; FILING DATE: 8-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3441 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 180..2441
US-08-525-864A-1

```

```

Query Match          74.3%;  Score 738.6;  DB 2;  Length 3441;
Best Local Similarity 90.4%;  Pred. No. 6.9e-183;
Matches 789;  Conservative 0;  Mismatches 84;  Indels 0;  Gaps 0;

```

```

Qy      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCTGCTCGCCTGC 60
        |||
Db      180 ATGAGGCGCGACCCGGCCCCCGGCTTCTCGATGCTGCTCTTCGGTGTGTCACTCGCCTGC 239

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db      240 TACTCGCCAGCCTCAAGTCCGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 299

Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db      300 GGCAAGGTACAGGGACTGGCCCCGGCAGGCGGTTCCAGCTCTAACAGCACCCGAGAGCCT 359

```

Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||
 Db 360 CCCGCCTCGGGTCGGGTGGCGCTGGTGAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 419
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 |||
 Db 420 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGCGCGCCGCTCGAAAGGAACCAG 479
 Qy 301 CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
 |||
 Db 480 CGCTACATCTTTTTCCTGGAGCCACCGAGCAGCCCTTAGTCTTTAAGACAGCCTTTGCC 539
 Qy 361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
 || |||
 Db 540 CCGGTCGACCCTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 599
 Qy 421 TGCGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
 |||
 Db 600 TGCGCAACCCGGCCCCAAGCTGAAGAAGATGAAGAGTCAGACAGGAGAGGTGGGCGAGAAG 659
 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
 || |||
 Db 660 CAGTCGCTCAAGTGTGAGGCGGCGGGGAACCCCGAGCCCTCCTATCGATGGTTCAAG 719
 Qy 541 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG 600
 || |||
 Db 720 GACGGCAAGGAGCTCAACCGAGTCGTGACATTCGCATCAAGTATGGCAACGGCAGAAAG 779
 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
 |||
 Db 780 AACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTGTGAG 839
 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
 || |||
 Db 840 GCTGAGAACATCCTTGGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGTGAGC 899
 Qy 721 ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 780
 |||
 Db 900 ACCACTCTGTCGTCCTGGTCGGGGCACGCCCCGGAAGTGCAATGAGACAGCCAAGTCCTAC 959
 Qy 781 TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
 || |||
 Db 960 TGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAGTGT 1019
 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 873
 || |||
 Db 1020 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 1052

RESULT 5

US-08-753-007A-3

; Sequence 3, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

Qy	731	CATCCTGGTCGGGGCACGCCC	GGAAGTGCAACGAGACAGCCAAGT	CCTATTGCGTCAATG	790
Db	362	CATCCTGGTCGGGACATGCCC	GGAAGTGCAATGAGACCGCCAAGT	CCTACTGTGTGAATG	421
Qy	791	GAGGCGTCTGCTACTACATCGAGGGC	ATCAACCAGCTCTCCTGCAAATGTCCAAATGGAT		850
Db	422	GAGGCGTGTGCTACTACATCGAGGGC	ATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT		481
Qy	851	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC			910
Db	482	TCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC			541
Qy	911	AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC			970
Db	542	AAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCAATGGTCAACTTCTC			601
Qy	971	CAAGCACCTTGGATTTGAATTAAA	994		
Db	602	CAAGCACCTTGGATTTGAATTGAA	625		

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;       TELEX:
;   INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 1476 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;       NAME/KEY: Coding Sequence
;       LOCATION: 69...1475
;   OTHER INFORMATION:
US-08-753-007A-7

```

```

Query Match          49.5%; Score 492; DB 3; Length 1476;
Best Local Similarity 92.8%; Pred. No. 9.1e-119;
Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
        || || | || | | | | | | | | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
        |||||
Db      158 AGCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
        |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
        |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
        |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
        |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

Qy      723 CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
        |||||
Db      458 CACCCTGTCATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517

Qy      783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
        |||||
Db      518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577

Qy      843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 902
        |||||
Db      578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 637

Qy      903 TCCTAAGCAAAGTGTC 918
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Db      638 TCCTAAGCAAAAAGCC 653

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RESULT 8

US-09-398-496-7

```
; Sequence 7, Application US/09398496
; Patent No. 6133423
; GENERAL INFORMATION:
;   APPLICANT: Gearing, David P.
;   APPLICANT: Busfield, Samantha J.
;   TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
;   TITLE OF INVENTION: AND USES THEREFOR
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson P.C.
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: US
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/398,496
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/753,007
;     FILING DATE: 19-NOV-1996
;     APPLICATION NUMBER: 08/699,591
;     FILING DATE: 19-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Fasse, J. Peter
;     REGISTRATION NUMBER: 32,983
;     REFERENCE/DOCKET NUMBER: 07334/022001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-542-5070
;     TELEFAX: 617-542-8906
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 1476 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY: Coding Sequence
;       LOCATION: 69...1475
;     OTHER INFORMATION:
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US-09-398-496-7

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Query Match          49.5%;  Score 492;  DB 3;  Length 1476;
Best Local Similarity 92.8%;  Pred. No. 9.1e-119;
Matches 516;  Conservative 0;  Mismatches 40;  Indels 0;  Gaps 0;
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Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397
 QY 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457
 QY 723 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 782
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 458 CACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTG 517
 QY 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 QY 843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 902
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 637
 QY 903 TCCTAAGCAAAGTGTC 918
 |||||||||||| |
 Db 638 TCCTAAGCAAAAAGGCC 653

RESULT 10

US-09-398-496-31

; Sequence 31, Application US/09398496

; Patent No. 6133423

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/398,496

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/753,007

; FILING DATE: 19-NOV-1996

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

Qy 903 TCCTAAGCAAAGTGTC 918
| | | | | | | | | | | |
Db 638 TCCTAAGCAAAAAGCC 653

RESULT 11

US-08-753-007A-1

; Sequence 1, Application US/08753007A

; Patent No. 6074841

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; APPLICANT: Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; TITLE OF INVENTION: AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/753,007A

; FILING DATE: 19-NOV-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2467 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: circular

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 79...1893

; OTHER INFORMATION:

US-08-753-007A-1

Query Match

47.1%; Score 467.8; DB 3; Length 2467;


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; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..394
US-08-525-864A-5
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Query Match          36.2%; Score 359.6; DB 2; Length 1207;
Best Local Similarity 94.0%; Pred. No. 2.7e-84;
Matches 374; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
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Qy      597 AAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTG 656
          |||
Db      1 AAAGAACTCACGGCTACAGTTCAACAAAGTGAAGGTGGAGGACGCTGGAGAGTACGTCTG 60

Qy      657 CGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGT 716
          |||
Db      61 TGAGGCTGAGAACATCCTTGGAAGGACACTGTGAGGGGCCGGCTCCATGTCAACAGTGT 120

Qy      717 GAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCCGAAGTGCAACGAGACAGCCAAGTC 776
          |||
Db      121 GAGCACCCTCTGTGCTCCTGGTCGGGGCACGCCCCGAAGTGCAATGAGACAGCCAAGTC 180

Qy      777 CTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAA 836
          |||
Db      181 CTA CTGTGTGAATGGAGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAA 240

Qy      837 ATGTCCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACAT 896
          |||
Db      241 ATGTCCAAACGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACAT 300

Qy      897 GCCAGATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCA 956
          |||
Db      301 GCCAGATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTCGCA 360

Qy      957 ATGGTCAACTTCTCCAAGCACCTTGGATTTGAATTAAA 994
          |||
Db      361 ATGGTCAACTTCTCCAAGCACCTTGGATTTGAATTAAA 398
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RESULT 14

US-08-525-864A-18

; Sequence 18, Application US/08525864A

; Patent No. 5912326

; GENERAL INFORMATION:

; APPLICANT: Chang, Han

; TITLE OF INVENTION: Cerebellum-derived Growth Factors, and Uses

; TITLE OF INVENTION: Related thereto

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AscII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,864A
; FILING DATE: 8-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-525-864A-18

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Query Match          13.6%; Score 135.6; DB 2; Length 142;
Best Local Similarity 97.2%; Pred. No. 2.8e-26;
Matches 138; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      792 AGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGATT 851
        ||||| ||||||||||||||| ||||||||||| ||||||||||||||||| |||||
Db      1 AGGCGTGTGCTACTACATCGAAGGCATCAACCAACTCTCCTGCAAATGTCCAAACGGATT 60

QY      852 CTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCA 911
        ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||
Db      61 CTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGCA 120

QY      912 AAGTGTCTGTGGGATACACCG 933
        |||||||||||||||||
Db      121 AAGTGTCTGTGGGATACACCG 142

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RESULT 15

US-08-036-555B-149

; Sequence 149, Application US/08036555B

; Patent No. 5530109

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

```

; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-036-555B-149

```

```

Query Match          9.6%; Score 95.4; DB 1; Length 1140;
Best Local Similarity 50.7%; Pred. No. 1.9e-15;
Matches 409; Conservative 0; Mismatches 361; Indels 37; Gaps 6;

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```

Qy      194 GGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGGGGGCTGCAGCGCG 253
        ||| |||| |   || || || || || || || || || ||
Db      11 GGGCGGCGAAAGCCGGGGGCTTGAAGAAGGACTCGCTGCTCACCGTGCGCCTGGGCGCCT 70
Qy      254 AGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAGCGCTACATCTTTT 313

```

Db	71	GGGGCCACCCCGCCTTCCCCTCCTGCGGGCGCCTCAAGGAGGACAGCAGGTACATCTTCT	130
Qy	314	TCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCCCCCTCGATACC-	372
Db	131	TCATGGAGCCCAGGCCAACAGCAGCGGCGGGCCCGCCGCCTTCCGAGCCTCCTTCCCC	190
Qy	373	-----AACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGC	423
Db	191	CCTCTCGAGACGGGCCGGAACCTCAAGAAGGAGGTGAGCCGGGTGCTGTGCAACGG-TGC	249
Qy	424	GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA	483
Db	250	GCCTTGCCTCCCCGCTTGAAAGAGATGAAGAGTCAGGAGTCTGTGGCAGGTTCCAAACTA	309
Qy	484	TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCCTACCGTTGGTTCAAGGAT	543
Db	310	GTGCTTCGGTGCGAGACCAGTTCTGAATACTCCTCTCTCAAGTTCAAGTGGTTCAAGAAT	369
Qy	544	GGCAAGGAGCTCAACCG---CAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	370	GGGAGTGAATTAAGCCGAAAGAACAAACCAGAAAACATCAAGATACAGAAAAGGCCGGGG	429
Qy	601	AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	430	AAGTCAGAACTTCGCATTAGCAAAGCGTCACTGGCTGATTCTGGAGAATATATGTGCAA	489
Qy	661	GCCGAGAACATCCTGGGGAAGGACA-----CCGTCCGGGGCCGGCTTTACGTCAACAGC	714
Db	490	GTGATCAGCAAACCTAGGAAATGACAGTGCCTCTGCCAACATCACCATTGTGGAGTCAAAC	549
Qy	715	GTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAG	774
Db	550	GCCACATCCACATCTACAGCTGGGACAAGCCATCTTGTCAAGTGTGCAGAGAAGGAGAAA	609
Qy	775	TCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTC----	830
Db	610	ACTTTCTGTGTGAATGGAGGCGAGTGCTTCATGGTGAAAGACCTTCAAATCCCTCAAGA	669
Qy	831	-----CTGCAAATGTCCAAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTG	885
Db	670	TACTTGTGCAAGTGCCAACCTGGATTCACTGGAGCGAGATGTACTGAGAATGTGCCCATG	729
Qy	886	CGATTGTACATGCCAGATCCTAAGCAAAGTGTCTGTGGGATACACCGGGGACAGGTGTC	945
Db	730	AAAGTCCAAA-----CCCAAGAAAAGTGCCCAAATGAGTTTACTGGTGATCGCTGCC	781
Qy	946	AGCAGTTCGCAATGGTCAACTTCTCCA	972
Db	782	AAAACCTACGTAATGGCCAGCTTCTACA	808

Search completed: August 15, 2004, 09:45:30
 Job time : 94.9371 secs

OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 08:02:19 ; Search time 536.161 Seconds
(without alignments)
9096.466 Million cell updates/sec

Title: US-09-864-675-1
Perfect score: 994
Sequence: 1 atgaggcgcgacccggccccc.....caccttggaattgaattaaa 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	994	100.0	994	9	US-09-864-675-1	Sequence 1, Appli
2	900	90.5	1884	14	US-10-096-241-5	Sequence 5, Appli
3	849	85.4	897	9	US-09-864-675-3	Sequence 3, Appli
4	547.2	55.1	1607	14	US-10-096-241-3	Sequence 3, Appli
5	492	49.5	1476	14	US-10-096-241-7	Sequence 7, Appli
6	492	49.5	2268	14	US-10-096-241-31	Sequence 31, Appl
7	467.8	47.1	2467	14	US-10-096-241-1	Sequence 1, Appli
8	424.8	42.7	22693	13	US-10-271-416-6	Sequence 6, Appli
9	424	42.7	1054	16	US-10-447-839A-10	Sequence 10, Appl
10	173	17.4	201	15	US-10-029-386-26613	Sequence 26613, A
11	173	17.4	419	16	US-10-447-839A-11	Sequence 11, Appl
12	173	17.4	573	15	US-10-029-386-12913	Sequence 12913, A
13	173	17.4	45450	13	US-10-271-416-7	Sequence 7, Appli
14	124.6	12.5	493	16	US-10-447-839A-12	Sequence 12, Appl
15	122.4	12.3	350	16	US-10-447-839A-13	Sequence 13, Appl
c 16	113.6	11.4	579	15	US-10-029-386-2532	Sequence 2532, Ap
c 17	111.8	11.2	171	15	US-10-029-386-16232	Sequence 16232, A
18	95.4	9.6	1140	8	US-08-736-019-149	Sequence 149, App
19	95.4	9.6	1140	10	US-09-366-886-55	Sequence 55, Appl
20	93.4	9.4	1193	8	US-08-736-019-134	Sequence 134, App
21	93.4	9.4	1193	10	US-09-366-886-3	Sequence 3, Appli
22	87	8.8	326	16	US-10-447-839A-14	Sequence 14, Appl
23	77.4	7.8	1986	10	US-09-373-658-71	Sequence 71, Appl
24	77.4	7.8	1986	11	US-09-989-687-71	Sequence 71, Appl
25	77.4	7.8	2003	8	US-08-736-019-21	Sequence 21, Appl
26	77.4	7.8	2003	10	US-09-366-886-71	Sequence 71, Appl
27	77.4	7.8	2003	10	US-09-373-658-72	Sequence 72, Appl
28	77.4	7.8	2003	11	US-09-989-687-72	Sequence 72, Appl
29	76.8	7.7	1108	8	US-08-736-019-135	Sequence 135, App
30	76.8	7.7	1108	10	US-09-366-886-5	Sequence 5, Appli
31	72.8	7.3	744	8	US-08-736-019-133	Sequence 133, App
32	72.8	7.3	744	10	US-09-366-886-1	Sequence 1, Appli
33	60.4	6.1	310	16	US-10-447-839A-15	Sequence 15, Appl
34	60.4	6.1	848	13	US-10-027-632-158930	Sequence 158930,
35	60.4	6.1	848	16	US-10-027-632-158930	Sequence 158930,
36	54.6	5.5	3272	12	US-10-152-319A-1922	Sequence 1922, Ap
37	52	5.2	1092	15	US-10-156-761-4747	Sequence 4747, Ap
38	52	5.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
39	50.6	5.1	3111	9	US-09-773-517-12	Sequence 12, Appl
40	50.6	5.1	3111	9	US-09-792-025-12	Sequence 12, Appl
41	50.6	5.1	3111	9	US-09-849-868-12	Sequence 12, Appl
42	50.6	5.1	3111	15	US-10-290-578-1	Sequence 1, Appli
43	50.6	5.1	3111	15	US-10-453-183-12	Sequence 12, Appl
44	49.8	5.0	1935	9	US-09-778-510-21	Sequence 21, Appl
45	49.8	5.0	1935	9	US-09-778-187B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-864-675-1

; Sequence 1, Application US/09864675

; Patent No. US20020081286A1

; GENERAL INFORMATION:

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; APPLICANT: Marchionni, Mark
; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS
; FILE REFERENCE: 04585/049002
; CURRENT APPLICATION NUMBER: US/09/864,675
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,495
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-675-1
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Query Match          100.0%; Score 994; DB 9; Length 994;
Best Local Similarity 100.0%; Pred. No. 1e-280;
Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60
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Db      1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 60

QY     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        |||
Db     61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120

QY    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
        |||
Db    121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180

QY    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
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Db    181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240

QY    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
        |||
Db    241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300

QY    301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
        |||
Db    301 CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

QY    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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Db    361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420

QY    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480
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Db    421 TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG 480

QY    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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Db    481 CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540

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Db	601		AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Qy	661		GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
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Qy	721		ACCACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
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Qy	781		TGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT	840
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Qy	841		CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA	900
Db	841		CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA	900
Qy	901		GATCCTAAGCAAAGTGTCCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTTCGCAATGG	960
Db	901		GATCCTAAGCAAAGTGTCCTGTGGGATACACCGGGGACAGGTGTCAGCAGTTTCGCAATGG	960
Qy	961		TCAACTTCTCCAAGCACCTTGGATTGAATTAAA	994
Db	961		TCAACTTCTCCAAGCACCTTGGATTGAATTAAA	994

RESULT 2

US-10-096-241-5

; Sequence 5, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

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;          CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
;     APPLICATION NUMBER: 08/699,591
;
;     FILING DATE: 19-AUG-1996
;
; ATTORNEY/AGENT INFORMATION:
;
;     NAME: Fasse, J. Peter
;
;     REGISTRATION NUMBER: 32,983
;
;     REFERENCE/DOCKET NUMBER: 07334/022001
;
; TELECOMMUNICATION INFORMATION:
;
;     TELEPHONE: 617-542-5070
;
;     TELEFAX: 617-542-8906
;
;     TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 5:
;
;     SEQUENCE CHARACTERISTICS:
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;         LENGTH: 1884 base pairs
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;         TYPE: nucleic acid
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;         STRANDEDNESS: single
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;         TOPOLOGY: linear
;
;     MOLECULE TYPE: cDNA
;
;     FEATURE:
;
;         NAME/KEY: Coding Sequence
;
;         LOCATION: 664...1883
;
;         OTHER INFORMATION:
;
;     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-096-241-5

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Query Match          90.5%;   Score 900;   DB 14;   Length 1884;
Best Local Similarity 99.3%;   Pred. No. 4.4e-253;
Matches 914;   Conservative 0;   Mismatches 5;   Indels 1;   Gaps 1;

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Db      218 ATGAGGCGCGACCCGGCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC 277

Qy      61 TACTCGCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
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Db      338 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 397

Qy      181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      398 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 457

Qy      241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
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Db      458 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 517

Qy      301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360
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Db      518 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 577

Qy      361 CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC 420
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 Qy 481 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 540
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 Db 697 CAATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG 756
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 Db 757 GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG 816
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 Qy 601 AACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG 660
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 Qy 661 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 720
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 Db 877 GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC 936
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 Db 937 ACCACCCTGTCATCCTGGTTCGGGGCACGCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT 996
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 Qy 781 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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 Db 997 TCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 1056
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 Qy 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 900
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 Db 1057 CCAAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCA 1116
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 Qy 901 GATCCTAAGCAAAGTGTCT 920
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 Db 1117 GATCCTAAGCAAAGCACCT 1136
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RESULT 3

US-09-864-675-3

; Sequence 3, Application US/09864675

; Patent No. US20020081286A1

; GENERAL INFORMATION:

; APPLICANT: Marchionni, Mark

; TITLE OF INVENTION: NRG-2 NUCLEIC ACID MOLECULES,

; TITLE OF INVENTION: POLYPEPTIDES, AND DIAGNOSTIC AND THERAPEUTIC METHODS

; FILE REFERENCE: 04585/049002

; CURRENT APPLICATION NUMBER: US/09/864,675

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/206,495

; PRIOR FILING DATE: 2000-05-23

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 897

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 85.4%; Score 849; DB 9; Length 897;
Best Local Similarity 98.3%; Pred. No. 3e-238;
Matches 858; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Qy	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAAGTGGCCGCTCCGGAGCGGG	240
Db	181	CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAAGTGGCCGCTCCGGAGCGGG	240
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Qy	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	301	CGCTACATCTTTTTCCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Qy	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Db	421	TGCGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAG	480
Qy	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Db	481	CAATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAG	540
Qy	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Db	541	GATGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAG	600
Qy	601	AACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Db	601	AACTCAGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAG	660
Qy	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Db	661	GCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGC	720
Qy	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780
Db	721	ACCACCCTGTCATCCTGGTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTAT	780

QY 781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGT 840
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 Db 781 TCGGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAGTGT 840
 QY 841 CCAAATGGATTCTTCGGACAGAGATGTTTGGAG 873
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 Db 841 CCTGTGGGATACACCGGGGACAGGTGTCAGCAG 873

RESULT 4

US-10-096-241-3

; Sequence 3, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1607 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 79...621


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; GENERAL INFORMATION:
;   APPLICANT: Gearing, David P.
;               Busfield, Samantha J.
;   TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES
;                       AND USES THEREFOR
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Fish & Richardson P.C.
;       STREET: 225 Franklin Street
;       CITY: Boston
;       STATE: MA
;       COUNTRY: US
;       ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/096,241
;       FILING DATE: 12-Mar-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/699,591
;       FILING DATE: 19-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Fasse, J. Peter
;       REGISTRATION NUMBER: 32,983
;       REFERENCE/DOCKET NUMBER: 07334/022001
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 617-542-5070
;       TELEFAX: 617-542-8906
;       TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1476 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;           NAME/KEY: Coding Sequence
;           LOCATION: 69...1475
;           OTHER INFORMATION:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-096-241-7

```

```

Query Match          49.5%; Score 492; DB 14; Length 1476;
Best Local Similarity 92.8%; Pred. No. 1.4e-133;
Matches 516; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
        || || | || | | | | ||| || | | || | |
Db      98  CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
        |||||||||||||||||||||||||||||||||||||||

```

Db 158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217
 Qy 483 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 218 ATCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277
 Qy 543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 602
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAGAAAGAA 337
 Qy 603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397
 Qy 663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457
 Qy 723 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTATTG 782
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 458 CACCCTGTCATCCTGGTTCGGGGCACGCCCCGGAAGTGCAACGAGACAGCCAAGTCTATTG 517
 Qy 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 Qy 843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 902
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGA 637
 Qy 903 TCCTAAGCAAAGTGTC 918
 ||||||||||| |
 Db 638 TCCTAAGCAAAAAGCC 653

RESULT 6

US-10-096-241-31

; Sequence 31, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/096,241
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,591
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 07334/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2268 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 69...2009
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-096-241-31

```

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Query Match          49.5%;  Score 492;  DB 14;  Length 2268;
Best Local Similarity 92.8%;  Pred. No. 1.6e-133;
Matches 516;  Conservative 0;  Mismatches 40;  Indels 0;  Gaps 0;

```

```

Qy      363 CCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTG 422
      || || | || | | | | || | | | | | | | | |
Db      98 CCGCGGCAAGAAGCACCCAGAGGGGAGGAAGCGGGAGAGGGAGCCCGATCCCGGGGAGAA 157

Qy      423 CGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 482
      |||||
Db      158 AGCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCA 217

Qy      483 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 542
      |||||
Db      218 ATCGCTGAAGTGTGAGGCAGCAGCCGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGA 277

Qy      543 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 602
      |||||
Db      278 TGGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAA 337

Qy      603 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 662
      |||||
Db      338 CTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGC 397

Qy      663 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 722
      |||||
Db      398 CGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCAC 457

```

Qy 723 CACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 782
 |||
 Db 458 CACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAGTCCTATTG 517
 Qy 783 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 842
 |||
 Db 518 CGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCC 577
 Qy 843 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 902
 |||
 Db 578 AAATGGATTCTTCGGACAGAGATGTTTGGAGAACTGCCTTTGCGATTGTACATGCCAGA 637
 Qy 903 TCCTAAGCAAAGTGTC 918
 |||
 Db 638 TCCTAAGCAAAAAGCC 653

RESULT 7

US-10-096-241-1

; Sequence 1, Application US/10096241

; Publication No. US20020127594A1

; GENERAL INFORMATION:

; APPLICANT: Gearing, David P.

; Busfield, Samantha J.

; TITLE OF INVENTION: DON-1 GENE AND POLYPEPTIDES

; AND USES THEREFOR

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,241

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/699,591

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fasse, J. Peter

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 07334/022001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2467 base pairs

```

;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: circular
;          MOLECULE TYPE: cDNA
;          FEATURE:
;            NAME/KEY: Coding Sequence
;            LOCATION: 79...1893
;            OTHER INFORMATION:
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-096-241-1

```

```

Query Match          47.1%; Score 467.8; DB 14; Length 2467;
Best Local Similarity 91.3%; Pred. No. 2e-126;
Matches 496; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```

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Qy      371 CCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 430
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2   CTAACGGCAAAAACATCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGACTGCGCCACCC 61

Qy      431 GGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAATCGCTGA 490
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62   GGCCCAAGCTGAAGAAGATGAAGAGCCAGACAGGAGAGGTGGGTGAGAAGCAGTCGCTCA 121

Qy      491 AGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGATGGCAAGG 550
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      122 AGTGTGAGGCAGCGGCGGAAACCCCCAGCCCTCCTATCGCTGGTTCAAGGATGGCAAGG 181

Qy      551 AGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAGAAAGAACTCACGAC 610
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      182 AACTCAACCGGAGTCGTGATATTTCGCATCAAGTATGGCAATGTGAGAAAGAACTCACGGC 241

Qy      611 TACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGTCTGCGAGGCCGAGAACA 670
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      242 TACAGTTCAACAAAGTGAGGGTGGAGGATGCCGGGGAGTACGTCTGTGAGGCCGAGAACA 301

Qy      671 TCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAGCGTGAGCACCACCCTGT 730
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      302 TCCTTGGGAAGGACACCGTGAGGGGCCGACTCCATGTCAACAGCGTGAGCACCACCTCTGT 361

Qy      731 CATCCTGGTCGGGGCAGCCCCGGAAGTGCAACGAGACAGCCAAGTCCTATTGCGTCAATG 790
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      362 CATCCTGGTCGGGACATGCCCGGAAGTGCAATGAGACCGCCAAGTCCTACTGTGTGAATG 421

Qy      791 GAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAATGGAT 850
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      422 GAGGCGTGTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGCAAATGTCCAAACGGAT 481

Qy      851 TCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC 910
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      482 TCTTCGGACAGAGATGTTTGGAGAAACTGCCTTTGCGATTGTACATGCCAGATCCTAAGC 541

Qy      911 AAA 913
          | | |
Db      542 AAA 544

```

US-10-271-416-6

; Sequence 6, Application US/10271416
; Publication No. US20040043021A1
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; APPLICANT: Little, Randall D.
; APPLICANT: Van Eerdewegh, Paul
; APPLICANT: Dupuis, Josee
; APPLICANT: Del Mastro, Richard G.
; APPLICANT: Allen, Kristina
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: 2976-4045
; CURRENT APPLICATION NUMBER: US/10/271,416
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/328,424
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22693
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-6

Query Match 42.7%; Score 424.8; DB 13; Length 22693;
Best Local Similarity 94.2%; Pred. No. 1.6e-113;
Matches 452; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

Qy	1	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	60
Db	20809	ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTGCGCTCGCCTGC	20868
Qy	61	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	120
Db	20869	TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG	20928
Qy	121	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGGCTCCAGCTCCAACAGCACCCGAGAGCCG	180
Db	20929	GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGGCTCCAGCTCCAACAGCACCCGAGAGCCG	20988
Qy	181	CCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	240
Db	20989	CCCGCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG	21048
Qy	241	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	300
Db	21049	GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG	21108
Qy	301	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	360
Db	21109	CGCTACATCTTTTTCTGGAGCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC	21168
Qy	361	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	420
Db	21169	CCCCTCGATACCAACGGCAAAAATCTCAAGAAAGAGGTGGGCAAGATCCTGTGCACTGAC	21228

Qy 421 TGC-GCCACCCGGCCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAA 479
 ||| | | || ||| | | ||| | || ||| ||||| |||||
 Db 21229 TGCGGTGAGTCGCCCCCTCCCTTTGCTGGAGAAAGGGGGGAGGGGCGAGGTGGTGGAGAA 21288

RESULT 9

US-10-447-839A-10

; Sequence 10, Application US/10447839A
 ; Publication No. US20040018181A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kufe, Donald W.
 ; APPLICANT: Kharbanda, Surender
 ; APPLICANT: Weitman, Steven D.
 ; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM
 ; FILE REFERENCE: 1000.05.009
 ; CURRENT APPLICATION NUMBER: US/10/447,839A
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: 10/293,391
 ; PRIOR FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 09/951,938
 ; PRIOR FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: 60/231,841
 ; PRIOR FILING DATE: 2000-09-11
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 10
 ; LENGTH: 1054
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-447-839A-10

Query Match 42.7%; Score 424; DB 16; Length 1054;
 Best Local Similarity 100.0%; Pred. No. 1e-113;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 60
 |||||
 Db 589 ATGAGGCGCGACCCGGCCCCCGGCTTCTCCATGCTGCTCTTCGGTGTGTCGCTCGCCTGC 648
 Qy 61 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 120
 |||||
 Db 649 TACTCGCCCAGCCTCAAGTCAGTGCAGGACCAGGCGTACAAGGCACCCGTGGTGGTGGAG 708
 Qy 121 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 180
 |||||
 Db 709 GGCAAGGTACAGGGGCTGGTCCCAGCCGGCGGCTCCAGCTCCAACAGCACCCGAGAGCCG 768
 Qy 181 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 240
 |||||
 Db 769 CCCGCCTCGGGTCGGGTGGCGTTGGTAAAGGTGCTGGACAAGTGGCCGCTCCGGAGCGGG 828
 Qy 241 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 300
 |||||
 Db 829 GGGCTGCAGCGCGAGCAGGTGATCAGCGTGGGCTCCTGTGTGCCGCTCGAAAGGAACCAG 888
 Qy 301 CGCTACATCTTTTTCCTGGAGCCCACGGAACAGCCCTTAGTCTTTAAGACGGCCTTTGCC 360

Db 147 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 199

RESULT 11

US-10-447-839A-11

; Sequence 11, Application US/10447839A

; Publication No. US20040018181A1

; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.

; APPLICANT: Kharbanda, Surender

; APPLICANT: Weitman, Steven D.

10 ; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED
11 THEREFROM

; FILE REFERENCE: 1000.05.009

; CURRENT APPLICATION NUMBER: US/10/447,839A

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: 10/293,391

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/951,938

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: 60/231,841

; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 109

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; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 11

; LENGTH: 419

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-447-839A-11

Query Match 17.4%; Score 173; DB 16; Length 419;

Best Local Similarity 100.0%; Pred. No. 2.7e-40;

Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483

Db 50 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 109

Ov 484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543

Db 110 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTC AAGGAT 169

QV 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTTCGCATCAAATATGGCAACGGCAG 596

Db 170 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 222

RESULT 12

US-10-029-386-12913

; Sequence 12913, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE

```

; TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
; FILE REFERENCE:  AEOMICA-X-2
; CURRENT APPLICATION NUMBER:  US/10/029,386
; CURRENT FILING DATE:  2001-12-20
; NUMBER OF SEQ ID NOS:  34288
; SOFTWARE:  Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12913
; LENGTH:  573
; TYPE:  DNA
; ORGANISM:  Homo sapiens
; FEATURE:
; OTHER INFORMATION:  MAP TO CHR5.3
; OTHER INFORMATION:  EXPRESSED IN HEART, SIGNAL = 0.55
; OTHER INFORMATION:  EXPRESSED IN ADULT LIVER, SIGNAL = 0.49
; OTHER INFORMATION:  EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION:  EXPRESSED IN BRAIN, SIGNAL = 0.66
; OTHER INFORMATION:  SWISSPROT HIT:  O14511, EVALUE 2.00e-28
; OTHER INFORMATION:  NT HIT:  AF119152.1, EVALUE 0.00e+00
; OTHER INFORMATION:  EST_HUMAN HIT:  BG996653.1, EVALUE 1.00e-108
US-10-029-386-12913

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Query Match          17.4%;  Score 173;  DB 15;  Length 573;
Best Local Similarity 100.0%;  Pred. No. 3e-40;
Matches 173;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      424  GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
          |||
Db      377  GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 436

Qy      484  TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
          |||
Db      437  TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 496

Qy      544  GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGGCAG 596
          |||
Db      497  GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGGCAG 549

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RESULT 13

US-10-271-416-7

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; Sequence 7, Application US/10271416
; Publication No. US20040043021A1
; GENERAL INFORMATION:
; APPLICANT:  Keith, Tim
; APPLICANT:  Little, Randall D.
; APPLICANT:  Van Eerdewegh, Paul
; APPLICANT:  Dupuis, Josee
; APPLICANT:  Del Mastro, Richard G.
; APPLICANT:  Allen, Kristina
; TITLE OF INVENTION:  NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION:  RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE:  2976-4045
; CURRENT APPLICATION NUMBER:  US/10/271,416
; CURRENT FILING DATE:  2002-10-11
; PRIOR APPLICATION NUMBER:  60/328,424
; PRIOR FILING DATE:  2001-10-11
; NUMBER OF SEQ ID NOS:  9

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 45450
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(45450)
; OTHER INFORMATION: n = A,T,C or G
US-10-271-416-7

Query Match 17.4%; Score 173; DB 13; Length 45450;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 483
|
Db 7026 GCCACCCGGCCCAAGTTGAAGAAGATGAAGAGCCAGACGGGACAGGTGGGTGAGAAGCAA 7085

Qy 484 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 543
|
Db 7086 TCGCTGAAGTGTGAGGCAGCAGCCGGTAATCCCCAGCCTTCCTACCGTTGGTTCAAGGAT 7145

Qy 544 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 596
|
Db 7146 GGCAAGGAGCTCAACCGCAGCCGAGACATTCGCATCAAATATGGCAACGGCAG 7198

RESULT 14

US-10-447-839A-12
; Sequence 12, Application US/10447839A
; Publication No. US20040018181A1
; GENERAL INFORMATION:
; APPLICANT: Kufe, Donald W.
; APPLICANT: Kharbanda, Surender
; APPLICANT: Weitman, Steven D.
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM
; FILE REFERENCE: 1000.05.009
; CURRENT APPLICATION NUMBER: US/10/447,839A
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 10/293,391
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/951,938
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,841
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-447-839A-12

Query Match 12.5%; Score 124.6; DB 16; Length 493;
Best Local Similarity 93.5%; Pred. No. 4.3e-26;

Matches 130; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy      594 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 653
      |||
Db      227 CAGAAAGAACTCACGACTACAGTTCAACAAGGTGAAGGTGGAGGACGCTGGGGAGTATGT 286

Qy      654 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 713
      |||
Db      287 CTGCGAGGCCGAGAACATCCTGGGGAAGGACACCGTCCGGGGCCGGCTTTACGTCAACAG 346

Qy      714 CGTGAGCACCACCCTGTCA 732
      || || ||| |||
Db      347 CGGTAGGTGGGCCCAGACA 365

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RESULT 15

US-10-447-839A-13

; Sequence 13, Application US/10447839A

; Publication No. US20040018181A1

; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.

; APPLICANT: Kharbanda, Surender

; APPLICANT: Weitman, Steven D.

; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM

; FILE REFERENCE: 1000.05.009

; CURRENT APPLICATION NUMBER: US/10/447,839A

; CURRENT FILING DATE: 2003-05-29

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; PRIOR APPLICATION NUMBER: 09/951,938

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: 60/231,841

; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 350

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-447-839A-13

Query Match 12.3%; Score 122.4; DB 16; Length 350;
 Best Local Similarity 99.2%; Pred. No. 1.7e-25;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      715 GTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAG 774
      |||
Db      99  GTGAGCACCACCCTGTCATCCTGGTCGGGGCACGCCCAGGAGTGAACGAGACAGCCAAG 158

Qy      775 TCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGC 834
      |||
Db      159 TCCTATTGCGTCAATGGAGGCGTCTGCTACTACATCGAGGGCATCAACCAGCTCTCCTGC 218

Qy      835 AAAT 838
      |||
Db      219 AAGT 222

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Search completed: August 15, 2004, 12:23:31
Job time : 545.161 secs